



SEQUENCE LISTING

<11> Rhodes, Kenneth
Betty, Maria
Ling, Hui-Ping
An, Wenqian

<12> POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

<13> MNI-070CP4

<14> USPN 09/070,756
<141> 2000-09-27

<15> USPN 60/110,277
<151> 1994-11-10

<15> USPN 60/110,033
<151> 1994-11-05

<15> USPN 60/109,333
<151> 1994-11-0

<15> USPN 09/036,731
<151> 1994-04-26

<15> USPN 09/050,614
<151> 1994-07-09

<15> USPN 09/050,874
<151> 1994-07-09

<15> USPN 09/060,492
<151> 1994-09-11

<15> USPN 09/089,913
<151> 1994-09-21

<15> PCT/US94/27428
<151> 1994-11-19

<16> 73

<17> PatentIn Ver. 2.1.0

<21> 1
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

tttctttcttcc	tccaatccag	agtagacaaa	ccacggggat	ttctttccag	ggtaggggag	180
gggaggagggc	gggggtacca	actgcgactc	aagttcttgc	tgac	atg ggg gcc gtc	236
					Met Gly Ala Val	
					1	
atg ggc acc ttc tca tct ctg caa acc aaa caa agg cga gcc tgg aaa	284					
Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys						
5 10 15 20						
gat aag att gaa gat gag ctg gag atg acc atg gtt tgc cat cgg ccc	332					
Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro						
25 30 35						
gag gga ctg gag cag ctg gag gcc cag acc aac ttc acc aag agg gag	380					
Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu						
40 45 50						
ctg cag gtc ctt tat cga gcc ttc aaa aat gag tgc ccc agt ggt gtg	428					
Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val						
55 60 65						
gtc aac gaa gac aca ttc aag cag atc tat gct cag ttc ttc cct cat	476					
Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His						
70 75 80						
gga gat gcc agc agg tat gcc cat tac ctg ttc aat gcc ttc gac acc	524					
Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr						
85 90 95 100						
act cag aca gcc tcc gtg aag ttc gag gac ttt gta acc gct ctg tgg	572					
Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser						
105 110 115						
att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat	620					
Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn						
120 125 130						
ttg tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg	668					
Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met						
135 140 145						
gac att gtc aaa gcc atc tat gac atg atg ggg aaa tac aca tat cct	716					
Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro						
150 155 160						
gty ttc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag	764					
Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln						
165 170 175 180						
aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt	812					
Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu						
185 190 195						
ttt att tta tta tta tta tta tta tta tta tta tta tta tta tta tta tta	860					
Gln Asn Val Met						

taataaadaa caacttaac aacctgatat gacctgttc tgattttata caacaaactct 972
 tgggaacagaa acacatttta caatttggaa gaattctctg ctgaagaatt tcttatggaa 1032
 cccagacata tcttggtcag tctctgattg ccaactcttc ctctttcttc ttcttgagag 1092
 agacaagatg aaatttgagt ttgttttggg agcatgctca tctctcaca ctgctgacct 1152
 atggaagpte cctctgctta agcttaacaa gtagtgacaa aaatatgctg cttactgccc 1212
 cccagccac tgcctacaag ccaggcagac ctgtgtgaat ctggaagcaa gaggacctga 1272
 gccagatgca caccatctct gatggccttc caaaccaatg tgcctgtttc tcttctttg 1332
 gtgggaagaa tgagagttat ccagaacaat taggatctgt catgaccaga ttgggagagc 1392
 cagcactaa catatgtggg ataggactga attattaagc atgacattgt ctgatgacct 1452
 aaactgcccc g 1463

c210: 2

c211: 216

c212: PRT

c213: Homo sapiens

c400: 2

Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg
 1 5 10 15

Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val
 20 25 30

Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
 35 40 45

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 50 55 60

Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
 65 70 75 80

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 85 90 95 100

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 105 110

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
 115 120 125

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Ser Gln Thr Thr Thr Thr

Tyr Thr Tyr Thr Val Ile Lys Ile Asp Thr Ile Asn Lys Thr Val Asp
 135 140 145 150

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
180 185 190

Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
195 200 205

Leu Gln Leu Phe Gln Asn Val Met
210 215

<210> 3

<211> 1856

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (300)..(1034)

<400> 3

ggcagacacac cccctggallc ttccggagaat atgcccgtgag gtgttgccaa ttattagtto 60

tcttggtctag cagatgttta gggactgggtt aagcccttgg agaaattacc ttaggaaaaac 120

ggggaaataa aagcaagat taccatgaat tgcaagatta cctagcaatt gcaaggtagg 180

agagagagagg tggagggcgg agtagacagg agggagggag aaagtgagag gaagcttaggc 240

ttgttgaaat aacccctgcac ttggaacagc ggcaagaag ccgcatttcc cagctttaa 299

atg cct gcc cgc gtt ctg ctt gcc tac ccg gga acg gag atg ttg acc 347

Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
1 5 10 15

cag gcc gag tct gaa ggg ctg cag acc ttg ggg ata gta gtg gtc ctg 395

Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
20 25 30

ctt tcc tct ctg aaa cta ctg cac tac ctg ggg ctg att gac ttg tcc 443

Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
35 40 45

gat gac aag atc gag gat gat ctg gag atg acc atg gtc tgc cac cgg 491

Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
50 55 60

ttt ttt gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga 539

Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
65 70 75 80

gaa ctg caa gtc ctt tac ccg gga ttc aaa aac gag tgc cac att ggt 597

Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
85 90 95

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 647

His Gly Arg Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn Ala Ile Asn

acc acc cag acc ggc tct gta aag ttc gag gac ttt gtg act gct ctg 731
 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
 130 135 140

tag att tta ctg aga gga acg gtc cat gaa aaa ctg agg tgg acg ttt 779
 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
 145 150 155 160

aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg 827
 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
 165 170 175

atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat 875
 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
 180 185 190

cct gtg ctc aaa gag gac act ccc agg cag cac gtg gac gtc ttc ttc 923
 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
 195 200 205

cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gac gaa ttc 971
 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
 210 215 220

ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg 1019
 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
 225 230 235 240

ttc caa aat gtc atg taactgagga caactggccat cctgctctca gagacactga 1074
 Phe Gln Asn Val Met
 245

caaacacctc aatgcoctga totgcocttg ttccagtttt acacatcaac totcgggaca 1134
 gaaatacctt ttacactttg gaagaattct ctgctgaaga cttctacaa aacctggcac 1194
 cgagtggctc agtctctgat tgcbaactct tctcctctcc tctctttgag agggacgagc 1254
 tgaaatccga agtttgtttt ggaagcatgc ccattctctc atgctgctgc tgcctgtggt 1314
 aaggccctc tgccttgagct taaacagtag tgcacagttt totgogtata cagatcccca 1374
 actcactgtt totaagtcag gcagacccctg atcaacttga accaaatgtg caccatcttc 1434
 gtagggatc ttaggcaat ggcctgctt ccttctctt ggtgcaaga aagaacttc 1494
 tacagagcac ttagagctta ccattgaaaat actgggagag gcagcaccta acacatgtat 1554
 aataggactg aattattaag catgggtggtc tcagatgatg caaagagccc atgctatttt 1614
 tcttccata gtagggat aattatttc cctctcttc acctatgac atagacaaag 1674
 cctctcttc

caaatacctt ttacactttg gaagaattct ctgctgaaga cttctacaa aacctggcac 1734
 cgagtggctc agtctctgat tgcbaactct tctcctctcc tctctttgag agggacgagc 1794
 tgaaatccga agtttgtttt ggaagcatgc ccattctctc atgctgctgc tgcctgtggt 1854
 aaggccctc tgccttgagct taaacagtag tgcacagttt totgogtata cagatcccca 1914
 actcactgtt totaagtcag gcagacccctg atcaacttga accaaatgtg caccatcttc 1974
 gtagggatc ttaggcaat ggcctgctt ccttctctt ggtgcaaga aagaacttc 2034
 tacagagcac ttagagctta ccattgaaaat actgggagag gcagcaccta acacatgtat 2094
 aataggactg aattattaag catgggtggtc tcagatgatg caaagagccc atgctatttt 2154
 tcttccata gtagggat aattatttc cctctcttc acctatgac atagacaaag 2214
 cctctcttc

<210> 4
 <211> 245
 <212> PRT
 <213> Rattus sp.

<400> 4

Met	Pro	Ala	Arg	Val	Leu	Leu	Ala	Tyr	Pro	Gly	Thr	Glu	Met	Leu	Thr
1				5					10					15	
Gln	Gly	Glu	Ser	Glu	Gly	Leu	Gln	Thr	Leu	Gly	Ile	Val	Val	Val	Leu
			20					25					30		
Cys	Ser	Ser	Leu	Lys	Leu	Leu	His	Tyr	Leu	Gly	Leu	Ile	Asp	Leu	Ser
		35					40					45			
Asp	Asp	Lys	Ile	Glu	Asp	Asp	Leu	Glu	Met	Thr	Met	Val	Cys	His	Arg
	50					55					60				
Pro	Glu	Gly	Leu	Glu	Gln	Leu	Glu	Ala	Gln	Thr	Asn	Phe	Thr	Lys	Arg
65					70					75					80
Glu	Leu	Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly
			85						90					95	
Val	Val	Asn	Glu	Glu	Thr	Phe	Lys	Gln	Ile	Tyr	Ala	Gln	Phe	Phe	Pro
			100					105					110		
His	Gly	Asp	Ala	Ser	Thr	Tyr	Ala	His	Tyr	Leu	Phe	Asn	Ala	Phe	Asp
		115					120					125			
Thr	Thr	Gln	Thr	Gly	Ser	Val	Lys	Phe	Glu	Asp	Phe	Val	Thr	Ala	Leu
	130					135					140				
Ser	Ile	Leu	Leu	Arg	Gly	Thr	Val	His	Glu	Lys	Leu	Arg	Trp	Thr	Phe
145					150					155					160
Asn	Leu	Tyr	Asp	Ile	Asn	Lys	Asp	Gly	Tyr	Ile	Asn	Lys	Glu	Glu	Met
			165					170					175		
Met	Asp	Ile	Val	Lys	Ala	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr
			180					185					190		
Pro	Val	Leu	Lys	Glu	Asp	Thr	Pro	Arg	Gln	His	Val	Asp	Val	Phe	Phe
	195						200					205			
Gln	Lys	Met	Asp	Lys	Asn	Lys	Asp	Gly	Ile	Val	Thr	Leu	Asp	Glu	Phe
	210					215					220				
Leu	Glu	Ser	Cys	Gln	Glu	Asp	Asp	Asn	Ile	Met	Arg	Ser	Leu	Gln	Leu
225					230					235					240
Phe	Gln	Asn	Val	Met											

11/1/81
 11/1/81
 11/1/81

<220>

<221> CDS

<222> (477)..(1124)

<400> 5

eggccccctg agatccagcc cagagcgcggy gcggagcggc cgggtggcag cagggggcggy 60
 cgggcgggagc gcagctcccg caccgcacgc ggcgcgggct cggcagccct ggccgtggcg 120
 gcacgcgggc ccgtgtccca acatcaggca ggctttgggg ctgggggctc ggccctcgga 180
 gaagccagtg gcccggctgg gtgcgcgac cggggggcgc ctgtgaagc tcccgcgagc 240
 ctctggccct gggagtcagt gcattgtgct ggtgaagaa ggcagcagc acgagctcca 300
 ggagcccggy cccacgctt totgaatac aagctgcagg cgagctgctc ggggcttttt 360
 tgctttctcg cttttctct cctcgaatc aaagtgggca atccacacg atttttttc 420
 aggggagggg agagacaggg cctggggctc caagacccac acaagtcttc gctgcc atg 479
 Met
 1

ggg gcc gtc atg ggc act ttc tcc tcc ctg cag acc aaa caa agg cga 527
 Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg
 5 10 15

ccc tct aaa gac aag att gag gat gag cta gag atg acc atg gtt tgc 578
 Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
 20 25 30

cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 629
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
 35 40 45

aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 671
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
 50 55 60 65

agc ggt gtg gtc aat gaa gaa aca ttc aag cag atc tac gct cag ttt 719
 Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 70 75 80

ttc cct cac gga gat gct agc aca tat aca tat tac ttc ttc aat gct 767
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
 85 90 95

ttc gac acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act 815
 Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr
 100 105 110

att ctg tgg att tta ctg aga ggg aca gtc cat gaa aaa cta agg tgg 863
 Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Arg Leu Ile Thr Thr

gag atg atg gac ata gtc aaa ggc atc tat gac atg atg ggg aaa tac 959
 Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr
 150 155 160

acc tat cct gtg ctc aaa gag gac act acc agg cag cat gtg gat gtc 1007
 Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val
 165 170 175

ttc ttc cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gat 1055
 Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp
 180 185 190

gaa ttt ctt gaa tca tgt cag gag gat gac aac atc atg aga tct cta 1103
 Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu
 195 200 205

cag ctg ttc caa aat gtc atg taactgagga caatggccat tctgctctca 1154
 Gln Leu Phe Gln Asn Val Met
 210 215

gagacactga caaacacott aatgcctga tctgccttg tcccaatttc acacaccaac 1214

tcttgggaca gaaatcactt ttacactttg gaagaattct ctgttgaaga ctttctacaa 1274

aacctggcac caagtggctc tgtctctgag ggaacgaggg agatccgact ttgttttggc 1334

agcatgcaca tctcttcctg ctgttgcctt gtggaaggcc cctctgcttg agcttaatca 1394

atagtgcaca gttttatgct taacatatat cccaaactcac tgcctccaag tcaggcagac 1454

tctgatgaat ctgagccaaa tgtgcacct cctccgatgg cctcccaagg caatgtgctt 1514

gctctctctt cctctggctgg aagaaagagt gttctacgga acaattagag cttaccatga 1574

aaatattggg agaggcagca cctaacacat gtagaatagg actgaattat taagcatggt 1634

gatatcagat gatgcacaatt gcccatgtca tttttttcaa aggtaggggac aaatgattct 1694

cccacaactag caactgttgt catagagcaa gtctctttaac atgcccagaa ggggaaccac 1754

tgtccagtgg tctatccctt ctctccatcc cctgtctcaa cccagcactg catgtccctt 1814

caagaaggct cagaatgctt gggaaagctt gtaatttat acatgctt aaataataaa 1874

caaacactat tgcacacaaa caaacacaaa aa 1934

<210> 6

<211> 216

<212> FRT

<213> Mus musculus

<400> 6

Tyr His Arg Thr Thr Tyr Leu Thr Thr Leu Thr Ala Thr Thr Ser Thr

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 50 55 60
 Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln
 65 70 75 80
 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 85 90 95
 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 100 105 110
 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
 115 120 125
 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 130 135 140
 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 145 150 155 160
 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
 165 170 175
 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
 180 185 190
 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
 195 200 205
 Leu Gln Leu Phe Gln Asn Val Met
 210 215

<10> 7
 <11> 1534
 <12> DNA
 <13> Rattus sp.

<120>
 <121> CDS
 <122> (31)..(711)

Met Gly Ala Val Met Gly Thr Phe
 1 5

Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp
 10 15 20

Ser Met Val Tyr His Arg Trp Lys Gly Lys Val Ile Leu His Ala Gln
 25 30 35 40 45

caaacagccc atgtcatttt ttttccagag gtagggacta ataattctcc cacactagca 1331
 cctacgatca tagaacaagt cttttaaac atccaggagg gaaacccgtg cccagtggtc 1391
 tctcccttct ctccatcccc tgcctaaagc cagcaactgc tgtctctccc ggaaggctca 1451
 gaatgcctgt gaaatgctgt aacttttata cccgtgtata atcaataaac agaactattt 1511
 cgtacaaaaa aaaaaaaaaa aaa 1534

<210> 3

<211> 227

<212> PRT

<213> Rattus sp.

<400> 2

Met	Gly	Ala	Val	Met	Gly	Thr	Phe	Ser	Ser	Leu	Gln	Thr	Lys	Gln	Arg
1				5						10				15	
Arg	Pro	Ser	Lys	Asp	Ile	Ala	Trp	Trp	Tyr	Tyr	Gln	Tyr	Gln	Arg	Asp
			20					25					30		
Lys	Ile	Glu	Asp	Asp	Leu	Glu	Met	Thr	Met	Val	Cys	His	Arg	Pro	Glu
		35					40					45			
Gly	Leu	Glu	Gln	Leu	Glu	Ala	Gln	Thr	Asn	Phe	Thr	Lys	Arg	Glu	Leu
	50					55					60				
Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	Val	Val
	65				70				75					80	
Asn	Glu	Glu	Thr	Phe	Lys	Gln	Ile	Tyr	Ala	Gln	Phe	Phe	Pro	His	Gly
				85					90					95	
Asp	Ala	Ser	Thr	Tyr	Ala	His	Tyr	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Thr
			100					105					110		
Gln	Thr	Gly	Ser	Val	Lys	Phe	Glu	Asp	Phe	Val	Thr	Ala	Leu	Ser	Ile
		115					120					125			
Leu	Leu	Arg	Gly	Thr	Val	His	Glu	Lys	Leu	Arg	Trp	Thr	Phe	Asn	Leu
	130					135					140				
Tyr	Asp	Ile	Asn	Lys	Asp	Gly	Tyr	Ile	Asn	Lys	Gln	Gln	Met	Met	Asp
145				150						155				160	
Ile	Val	Lys	Ala	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Val
			165						170					175	
Leu	Lys	Glu	Asp	Thr	Pro	Arg	Gln	His	Val	Asp	Val	Phe	Phe	Gln	Lys
			180				185								

... ..

Asn Val Met
225

<210> 9
<211> 1540
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> 77)..(757)

<400> 9
atccacacccg attttttttt aggggaggga agagacaggg cctgggggtcc caagacgcac 60
aaagtcttc gctgcc atg ggg gcc gtc atg ggc act ttc tcc tcc ctg cag 112
Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln
1 5 10
acc aaa caa agg cga ccc tct aaa gac atc gcc tgg tgg tat tac cag 160
Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp Trp Tyr Tyr Gln
15 20 25
tat cag aga gac aag att gag gat gag cta gag atg acc atg gtt tgc 208
Tyr Gln Arg Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
30 35 40
cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 256
His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
45 50 55 60
aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 304
Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
65 70 75
agc ggt gtg gtc aat gaa gaa aca ttc aag cag atc tac gct cag ttt 352
Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
80 85 90
ttc cct cac gga gat gcc agc aca tat gca cat tac ctc ttc aat gcc 400
Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
95 100 105
ttc gac acc acc cac aca ggt tct gta aag ttc agc tat ttc ttc acc 448
Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr
110 115 120
gct ctg tgc att tta ctg aga ggg aca gtc cat gaa aaa cta agg tgg 496
Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp
125 130 135 140
acg ttt aat ttg tat gac ttc tat acc acc acc tat cta acc acc acc 544
Thr Phe Ile Thr Val Val Val Val Val Val Val Val Val Val Val Val
145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

atccacacacccg attttttttt aggggaggga agagacaggg cctgggggtcc caagacgcac 60
aaagtcttc gctgcc atg ggg gcc gtc atg ggc act ttc tcc tcc ctg cag 112
Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln
1 5 10
acc aaa caa agg cga ccc tct aaa gac atc gcc tgg tgg tat tac cag 160
Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp Trp Tyr Tyr Gln
15 20 25
tat cag aga gac aag att gag gat gag cta gag atg acc atg gtt tgc 208
Tyr Gln Arg Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
30 35 40
cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 256
His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
45 50 55 60
aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 304
Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
65 70 75
agc ggt gtg gtc aat gaa gaa aca ttc aag cag atc tac gct cag ttt 352
Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
80 85 90
ttc cct cac gga gat gcc agc aca tat gca cat tac ctc ttc aat gcc 400
Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
95 100 105
ttc gac acc acc cac aca ggt tct gta aag ttc agc tat ttc ttc acc 448
Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr
110 115 120
gct ctg tgc att tta ctg aga ggg aca gtc cat gaa aaa cta agg tgg 496
Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp
125 130 135 140
acg ttt aat ttg tat gac ttc tat acc acc acc tat cta acc acc acc 544
Thr Phe Ile Thr Val Val Val Val Val Val Val Val Val Val Val Val
145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

acc tat cct gtg ctc aac gag gac act tcc aca cag cat gtg gac gtc 640
Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val
175 180 185

ttc ttc gag aaa atg gat aaa aat aaa gat ggc att gta acg tta gat 698
Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp
190 195 200

gaa ttt ctt gaa tca tgt bag gag gat gac aac atc atg aga tct cta 736
Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu
205 210 215 220

gag ctg ttc aag aat gtc atg taactgagga cactggccat tctgctctca 787
 Gln Leu Phe Gln Asn Val Met
 225

```

gagacactga caaacacott aatgcocctga tetgcoccttg ttccaatttt acacaccaac 847
tcttggggaca gaaataacott ttacaacttg gaagaattct ctgctgaaga cttttctacaa 907
aacctggcac cactgggctc tgtctctgag ggaagagcgg agatccgact ttgttttgga 967
agcatgcaca tctcttcctg ctgctgcocct gtggaaggcc cctctgcttg agcttaacta 1027
atagtgacaa gttttatgct tacacatata cccaaactac tgcctccaag tcaggcagac 1087
cttgatgaat ctgagccaaa tgtgcaccat cctccgatgg cctcccaagg caatgtgcct 1147
gcttctcttc ccttggttgg aagaaaagagt gttctacgga accaattagag cttaccatga 1207
aaatattggg agaggcagca cctaacacat gtagaatagg actgaattat taagcatggt 1267
gatatcagat gatgcaaaat gcccatgtca tttttttcaa aggtagggac aaatgattct 1327
cccacactag caactgttgt catagagcaa gtctcttaac atgcocagaa ggggaaccac 1387
tgtccagtgg totatccctc ctctccatcc cctgctcaaa cccagcactg catgtccctc 1447
caagaaggtc cagaatgcct gcgaaaacgt gtacttttat accctgttct aatcaataaa 1507
cagaactatt tcgtacaaaa aaaaaaaaaa aaa 1540

```

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

```

4400> 10
Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg
      1             5             10             15

```

Arg Pro Ser Lys Asp Ile Ala Thr Tyr Phe Thr Thr Ile Thr Glu Asn Lys

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val
65 70 75 80

Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
85 90 95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
100 105 110

Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser Ile
115 120 125

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
130 135 140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Val
165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu Glu
195 200 205

Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe Gln
210 215 220

Asn Val Met
225

<110> 11
<111> 955
<112> DNA
<113> Rattus sp.

<120>
<121> CDS
<122> (345)..(953)

<210>
<211> misc feature
<212> 619
<213> n,a,c,g, or t

<210>
<211> VARIANT
<222> 92 of the corresponding amino acid
<223> X=any amino acid

ctaggatggtt ggaaataaac ctgcacttgg aacagcggca aagaagcggg attttcragc 300
 tttaaatgac tgcacgggtt ctgcttggct acccgggaac ggag atg ttg acc gag 356
 Met Leu Thr Gln
 1
 ggc gag tct gaa ggg ctc cag acc ttg ggg ata gta gtg gtc ctg tgt 404
 Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu Cys
 5 10 15 20
 tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tcc gat 452
 Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser Asp
 25 30 35
 gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg cct 500
 Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg Pro
 40 45 50
 gag gga ctg gag gag ctt gag gca gag acg aac ttc acc aag aga gaa 548
 Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
 55 60 65
 ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt gtg 596
 Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val
 70 75 80
 gtt aac gaa gag aca ttc aag cng atc tac gct cag ttt ttc cct cat 644
 Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln Phe Phe Pro His
 85 90 95 100
 gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac acc 692
 Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
 105 110 115
 acc cag aca ggc tct gta aag ttc gag gac ttt gtg act gct ctg tcc 740
 Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
 120 125 130
 att tta ctg aga gga acg gtc cat gaa aaa ctg aag tgg acg ttt aat 788
 Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys Trp Thr Phe Asn
 135 140 145
 ttg tac gac atc cat aaa gac ggc tac ata aac aac gac gac atg atg 836
 Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Gln Gln Met Met
 150 155 160
 gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat ctt 884
 Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Leu
 165 170 175 180
 gta ctc aaa gac tat atc ttc agc gag gac gta gac gta ttc ttc cag 932
 Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Arg Thr Thr Thr Thr

<211> 203
 <212> PRT
 <213> Rattus sp.

<220>
 <221> VARIANT
 <222> 92
 <223> Xaa=any amino acid

<400> 12
 Met Leu Thr Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val
 1 5 10 15
 Val Val Leu Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile
 20 25 30
 Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
 35 40 45
 Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
 50 55 60
 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 65 70 75 80
 Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln
 85 90 95
 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 100 105 110
 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 115 120 125
 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
 130 135 140
 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 145 150 155 160
 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 165 170 175
 Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
 180 185 190
 Val Ile Phe Gln Lys Met Asp Lys Asn Lys Asp
 195 200

<210> 13
 <211> 1134
 <212> RNA

1

5

10

15

22

23

3:1

55

40

$$1 =$$

51

55

60

65

70

75

32

35

37

35

17.

10

110

115

120

125

130

135

7 4 3

145

150

55

50

15"

• 1000

225

100

1000

10

10

cct gga ctc cgg gag gag gcc cca agg gaa caa gtg gag agc ttc ttc 908
 Pro Ala Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe
 220 225 230
 cag aag atg gac aga aac aag gat ggt gtg gtg acc att gag gaa ttc 953
 Gln Lys Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe
 235 240 245
 att gag tct tgt caa aag gat gag aac atc atg agg tcc atg gag ctc 1001
 Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu
 250 255 260 265
 ttt gac aat gtc atc tagccccag gagagggggg cagtgtttcc tgggggggacc 1056
 Phe Asp Asn Val Ile
 270
 atgctctaac cctagtcacag ggggaacctca cctttctctt cccaggctca tcttcactct 1116
 acgcctccct gggggctgga gggatccaaag agcttggggg ttcagtagtc cagatctctg 1176
 gagctgaagg ggccagagag tgggcagagt gcctctcggg ggggtgttccc aactcccacc 1236
 agctctcacc ccttctctgc ctgacaccca gtgttgagag tgcctctctt gtaggaattg 1296
 agcgggtccc cactctctac cctactctag aaacacacta gagcgatgtc tctgctatg 1356
 gtgcttcccc cactcctgac ctacataaaca ttctccctaa gactcccttc tcagagagaa 1416
 tgcctcattc tgggaactgg ctggcttctc agaccagcca ttgagagccc tgtgggaggg 1476
 ggacaagaat gtatagggag aaatcttggg cctgagtcac tggataggtc ctaggaggtg 1536
 ggtgggggtt agaatagaag ggcttggaac gattatgatt gctcaggaat accaggttat 1596
 agctccaagt tcacaggtc tgcatacaca ggccatcaaa atataagttt ccaggctttg 1656
 cagaagacct tgtctcctta gaaatgcctc agaaattttt cacaccttc tgggtatcca 1716
 tggagagcct ggggcacagat atctggctca tctctggcat tgcctctctt ccttctcttc 1776
 tgcctgtgtt ggtggtggtt gtggtggggg aatgtggatg ggggatgttc tgctgatgc 1836
 ctgcaaaaat ttcatccac cctccttggc tatctctctt gtttgaggg ctatgacttg 1896
 ggtttgtt tccatgttt ctatagatt tgggtttt ctgaaattg ggtttatca 1956
 tcccccacagt ggtgcctta gaaggagag ggaaggagg aggcaggaat agc 2009

<210> 14

<211> 270

<212> 187

<213> 187-188-189-190

Arg Gly Ala Gly Arg Ala Leu Thr Arg His Leu Leu Arg Ile Thr Ile

Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

0.220
0.000, 0.000

Pro	Ser	Lys	Lys	Ala	Leu	Lys	Gln	Arg	Phe	Leu	Lys	Leu	Leu	Pro	Cys	
			20					25						30		
tgc	ggg	ccc	caa	gcc	ctg	ccc	tca	gtc	agt	gaa	aca	tta	gct	gcc	cca	145
Cys	Gly	Pro	Gln	Ala	Leu	Pro	Ser	Val	Ser	Glu	Thr	Leu	Ala	Ala	Pro	
		35					40					45				
gcc	tcc	ctc	agg	ccc	cac	aga	ccc	ggc	ccg	ctg	gac	cca	gac	agg	gta	193
Ala	Ser	Leu	Arg	Pro	His	Arg	Pro	Arg	Pro	Leu	Asp	Pro	Asp	Ser	Val	
	50					55					60					
gag	gat	gag	ttt	gaa	tta	tcc	acg	gtg	tgt	cac	cga	cct	gag	ggc	ctg	241
Glu	Asp	Glu	Phe	Glu	Leu	Ser	Thr	Val	Cys	His	Arg	Pro	Glu	Gly	Leu	
	65				70				75						80	
gaa	caa	ctc	cag	gaa	cag	acc	aag	ttc	aca	cgc	aga	gag	ctg	cag	gtc	289
Glu	Gln	Leu	Gln	Glu	Gln	Thr	Lys	Phe	Thr	Arg	Arg	Glu	Leu	Gln	Val	
			85					90						95		
ctg	tac	cga	ggc	ttc	aag	aac	gaa	tgc	ccc	agt	ggg	att	gtc	aac	gag	337
Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	Ile	Val	Asn	Glu	
			100					105					110			
gag	aac	ttc	aag	cag	att	tat	tct	cag	ttc	ttt	ccc	caa	gga	gac	tcc	385
Glu	Asn	Phe	Lys	Gln	Ile	Tyr	Ser	Gln	Phe	Phe	Pro	Gln	Gly	Asp	Ser	
	115						120					125				
agg	aac	tat	gct	act	ttt	ctc	ttc	aat	gcc	ttt	gac	acc	aac	cac	gat	433
Ser	Asn	Tyr	Ala	Thr	Phe	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Asn	His	Asp	
	130					135					140					
ggc	tct	gtc	agt	ttt	gag	gac	ttt	gtg	gct	ggc	ttg	tgc	gtg	att	ctt	481
Gly	Ser	Val	Ser	Phe	Glu	Asp	Phe	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu	
145					150				155					160		
cgg	ggg	acc	ata	gat	gat	aga	ctg	agc	tgg	gct	ttc	aac	tta	tat	gac	529
Arg	Gly	Thr	Ile	Asp	Asp	Arg	Leu	Ser	Trp	Ala	Phe	Asn	Leu	Tyr	Asp	
			165					170					175			
ctc	aac	aag	gac	ggc	tgt	atc	aca	aag	gag	gaa	atg	ctt	gac	att	atg	577
Leu	Asn	Lys	Asp	Gly	Cys	Ile	Thr	Lys	Glu	Glu	Met	Leu	Asp	Ile	Met	
		180						185					190			
aag	tcc	atc	tat	gac	atg	atg	ggc	aag	tac	aca	tac	cct	gac	ctc	cgg	625
Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Ala	Leu	Arg	
	195						200					205				
gag	gag	gac	cca	aga	gaa	cac	gtg	gag	agg	ttc	ttc	cag	aag	atg	gac	673
Glu	Glu	Ala	Pro	Arg	Glu	His	Val	Glu	Ser	Phe	Phe	Gln	Lys	Met	Asp	
	210					215					220					
agg	aac	aag	gac	ggc	ttt	gtg	acc	atc	gag	gaa	ttc	atc	gac	tat	ttt	721
Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe	Ile	Glu	Ser	Cys	
225					230						235					

tccagtgaca gacgaaccta accctctctc tccaggatcg tcccatcttt accgtgaccc 982
 tgggggctgt agggattcaa taccctgggg cttcagtagt ccagatccct gagctaagtc 942
 acaaaagtag gcaagagtag gcaagctaaa tctggggggt tcccaacccc ccagagctct 1002
 caccctctct caactgatac ctagtgtgga ggaacacct ggtgtaggga ccaagtgggt 1062
 ctccaccttc tagtcccaat ctagaaacca cattagacag aaggtctctt gctatgggtc 1122
 ttcccccata cctaattctt tagatttttc tcaagactcc cttctcagag aacacgctct 1182
 gtccatgtcc ccagctgggg acatggacag agcgtgttct ctagttctag atcgcgagcg 1242
 gcgga 1247

<210> 16
 <211> 257
 <212> PRT
 <213> Rattus sp.

<400> 16
 Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly
 1 5 10 15
 Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys
 20 25 30
 Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
 35 40 45
 Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
 50 55 60
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 65 70 75 80
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 85 90 95
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 100 105 110
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 115 120 125
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 130 135 140
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 145 150 155 160
 Lys Ser Ile Tyr Asp Met Met Gly Lys Pro Thr Tyr Pro Ala Ile Arg

Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp
210 215 220

Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys
225 230 235 240

Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val
245 250 255

Ile

0210: 17

0211: 2343

0212: DNA

0213: Mus musculus

0220:

0221: CDS

0222: (131)..(990)

0400: 17

agggaactctg aggtggggccc taaaatccag cgctcccccag agaaaagcct tgcagagccc 60

tactccgggc cccagagccc agcaggctgc tgcgcgcga gggggcactg tctgagagccc 120

ctatcttggc caccgggggc cccctccccc ggcccaggcg ggaggggggc gcgggggggc 180

atg ggg ggc caa ggc cga aag gag agt ttg tcc gaa tcc cga gat ttg 228
Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
1 5 10 15

gac ggc tcc tat gac cag ctt acg ggc cac cct cca ggg ccc agt aaa 276
Arg Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
20 25 30

aaa gcc ctg aag cag cgt ttc ctc aag ctg ctg ccg tgc tgc ggg ccc 324
Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
35 40 45

caa gcc ctg ccc tca gtc agt gaa aca tta ggt gcc cca gcc tcc ctc 372
Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
50 55 60

cga cca cac aga gcc cgc ccg ctg gac cca gac agc gtg gag gat gag 420
Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
65 70 75 80

ttt gaa cta tcc acg ctg tcc cac ccg cct tat agt ctc caa caa ctc 468
Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu
85 90 95

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 54
Phe Phe Lys Asn His Cys Pro Ser Gly Ile Val Asn His His Asn Phe

aag aaa att tat tct cag ttc ttt ccc caa gga gac tcc agc aac tac 612
 Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr
 130 135 140

gat aat ttt ctc ttc aat gcc ttt gac acc aac cat gat ggc tct gtc 660
 Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
 145 150 155 160

agt ttt gag gac ttt gtg gct ggt ttg tca gtg att ctt agg gga acc 708
 Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Trp
 165 170 175

ata gat gat aga ctg aac tgg gct ttc aac tta tat gac ctc aac aag 756
 Ile Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
 180 185 190

gat ggc tgt atc acg aag gag gaa atg ctc gac atc atg aag tcc atc 804
 Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
 195 200 205

tat gac atg atg ggc aag tac acc tac cct gcc ctc cgg gag gag gcc 852
 Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
 210 215 220

cng agg gaa cac gtg gag agc ttc ttc cag aag atg gac aga aac aag 900
 Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
 225 230 235 240

gac gcc gtg gtg acc att gag gaa ttc att gag tct tgt caa cag gac 948
 Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
 245 250 255

gag aac atc atg agg tcc atg caa ctc ttt gat aat gtc atc 990
 Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

tagctcccca gggagagggg ttagtgtgtc ccagggtaac catgctgtag cctagttcca 1050
 gtcaaaccta accctctctt ccccggtct gtctcctcc tacctgtacc ctgggggctg 1110
 tagggattca acatcctggc gcttcagtag tccagatccc tgagctaaat ggcgagagta 1170
 ggaagctaa ctcttttgaat gctggttggg gagggtcaca ttcagatcc agagagatc 1230
 tccac cttc ctgactgat accagatct gaggta cc ctatctctg gagggtc 1290
 agtggttctc tgcctcccca gccactcta gagaccaca ctgacggga atatctctg 1350
 ctatggtgtt tcccccctcc ctgacggcag attttctctc taagactccc ttctcagaga 1410
 ctatgctttt gctcttggc ctgggttggg ttctctgct agctttgag gacctctgt 1470

ttaggatcca gatgtccggt ccattccctga aacctctccc tccctccctgc tccctatggtg 1770
 ggagtgggtg ccaggggaag atgagtgagc cgggtgctctg gatgatgcct gtaagggtcc 1830
 acctacct ccggtctgca agccgtctctg gtgacctcgt ttgattctcc atgacctctg 1890
 ctatgatgta gaggtgtgga gtgagttctag tggcagcctt aggggaatgg gaagaacgag 1950
 cgggcactc cactgaacc cagtgtgggg gcattccattc gaatctttgc ctggtctccc 2010
 caatgcctt aggtatctct agggctccca cccccactct ttagtctacc cagagatgct 2070
 cagagctca cctagagggc agggaccata ggtccaggt ccaactgtc atcagcatcc 2130
 ggcattctg ctgtctgctta ttaataaac ttgcttctctt ccagcgcccc tccccagtc 2190
 ggcaggtct gaggggaagg cccccaactt cccgcctcct gtcagacatt gttgactgct 2250
 ttgcatcttg ggcctctcta cctatatttt gtataataag aagacacca gatccaataa 2310
 aacacatggc taagcacaaa aaaaaaaaaa aaa 2343

#10: 18
 #11: 270
 #12: PRT
 #13: Mus musculus

#100: 18
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
 50 55 60
 Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
 65 70 75 80
 Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Glu Leu
 85 90 95
 Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
 100 105 110
 Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asp Ile
 115 120 125
 Ser Thr Glu Arg Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Ile Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
 180 185 190

Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
 195 200 205

Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
 210 215 220

Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
 225 230 235 240

Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
 245 250 255

Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

*Q100: 19
 *Q110: 1955
 *Q120: DNA
 *Q130: Homo sapiens

*Q120:
 *Q210: CDS
 *Q220: (207)..(962)

*Q400: 19
 ctacactgct gactagtgtt cctctctctg ctccaggacc tccgggtaga cctcagacac 60
 cgggccatt cccagactca gctcagccc ggactccccc agccccgaca gcacagttag 120
 cggccagggg gggcgtgtg agcgcctat cccggccacc cggcgcctcc tcccagggc 180
 cggcggggag cgggggcgcg ggggac atg cgg ggc cag ggc cgc aag gag agt 233
 Met Arg Gly Gln Gly Arg Lys Glu Ser
 1 5

ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac cag ctg acg ggc 281
 Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
 10 15 20 25

gac tcc tcc tcc ccc gac tcc tcc tcc tcc tcc tcc tcc tcc tcc tcc 331
 His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys
 30 35 40

ctg ctg cgg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt gaa aac 377
 Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
 45 50 55

agg gtc gat gat gaa ttt gaa ttt ttt ttt ttt ttt ttt ttt ttt ttt 427
 Arg Val Asp Asp Gaa ttt gaa ttt ttt ttt ttt ttt ttt ttt ttt ttt
 430 435 440 445 450 455 460 465 470 475

*Q100: 19
 *Q110: 1955
 *Q120: DNA
 *Q130: Homo sapiens

*Q120:
 *Q210: CDS
 *Q220: (207)..(962)

Journal of Management Education 36(8) 907-924
© The Author(s) 2012. Reprints and permissions:
<http://www.sagepub.com/journalsPermissions.nav>

agctccaaagt tccacagggtc tgcataccaca ggccatcaaa atataagtt ccaggctttg 1602
 cagaagacct tgtctcccta gaaatgcccc agaaatttc cacacutcc tgggtatcca 1662
 tggagagacct ggggcccagat atctggctca tctctggcat tgccttctct ccttccctcc 1722
 tgcagtgttt ggagggtggtt gtggtggggg aatgtggatg ggggatgtcc tggctgatgc 1782
 ctgcacaaaat ttatccccc cctccttgct tatcgctcct gttttgaggg ctatgacttg 1842
 aatttttgtt tccatgttc tctatagact tgggaccttc ctgaacttgg ggccatccac 1902
 tccccacagt ggatgcctta gaagggagag ggaaggaggg aggcaggcat agc 1955

<L10> 20
 <L11> 252
 <L12> PRT
 <L13> Homo sapiens

<400> 20
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Thr Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Asp Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 115 120 125
 Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 145 150 155 160
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 165 170 175

<L14> 20
 <L15> 252
 <L16> PRT
 <L17> Homo sapiens

<400> 20
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu

acc aac cac gat ggc tct gtc agt ttt gag gac ttt gtg got ggt ttg 666
Thr Asn His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu
140 145 150

tgg gtg att ctt cgg ggg acc ata gat gat aga ctg agc tgg got ttc 714
Ser Val Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe
155 160 165

aac tta tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg 762
Asn Leu Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met
170 175 180

ctt gac att atg aag tcc atc tat gac atg atg ggc aag tac aca tac 810
Leu Asp Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
185 190 195

cct gcc ctc cgg gag gag gcc cca aga gaa cac gtg gag agc ttc ttc 858
Pro Ala Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe
200 205 210 215

cag aag atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc 906
Gln Lys Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe
220 225 230

atc gag tct tgt cca cag gac gag aac atc atg agg tcc atg cag ctc 954
Ile Glu Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu
235 240 245

ttt gat aat gtc atc tagctcccca gggagagggg ttagtgtgtc ctagggtgac 1009
Phe Asp Asn Val Ile
250

caggctgtag tcttagtcca gaaggaaccta acctctcttc tccaggcctg tctcatttt 1059

acctgtaccc tgggggctgt agggattcaa tctctgggg cticagtagt ccagatccct 1129

gagctaagtc acaaaagtag gcaagagtag gcaagctaaa tctgggggct tcccaacccc 1189

cgacagctct caccctctct caactgatac ctagtgtgta ggacacccct ggtgtaggga 1249

ccaagtgggt ctccaccttc tagtccact ctagaaacca cattagacag aaggtctcct 1309

gotatgggtgc ttcccccata cctaattctct tagatttcc tcaagactcc ctctcagag 1369

aacacctctt gtccatgttc ccagcttct tctcacta gctctgag; aggtgtgg 1429

gagggggg; cagaaagaa gaaaagtctt ggcctcagag cagtgggttag gtccaggaa 1489

ttggctggag tggaggccag aaagcctggg cagatgatga gagccagct gggctgtcac 1549

tgcaggttcc ggggcctaca gccctgggtc agcagatgat gaggccca; actttccaga 1609

aggtcccttag caatgtccca gaaattcaga gaaattctt cagtctttt ggggtcttcc 1669

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 1729

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 1789

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 1849

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 1909

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 1969

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2029

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2089

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2149

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2209

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2269

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2329

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2389

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2449

gaggtctctt ggtctcttct ggtctcttct ggtctcttct ggtctcttct ggtctcttct 2509

aggggaatgg; gaagaaaccca atgtggggggc acccattaga atcttggccc ggctccctcac 1969
 aatgccttag ggctcccttag ggtaccggct cctctgtttt agtatacca gagatgctcc 2029
 ttagctcacc tagagggttag ggaagggttag ctccaggtcc aacctctcca ggctcagcacc 2089
 ctggcatgct gctgctctctc attaacaacac ctgcttgtct cctctctgccc cctttctcag 2149
 tcagccaggg tctgaggggga agggcctccc gtttccccc ccttcagaca tgggtgactg 2209
 ctttgcattt tggctctctc tatctatttt gtaaaataag acatcagatc caataaaaca 2269
 cacgctatg caaaaaaaaa aaaaaaaaaa a 2300

<210> 22
 <211> 252
 <212> PRT
 <213> Rattus sp.

<400> 22
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
 145 150 155 160
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asn Leu Ser Ser Ser Thr
 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

Glu His Val Glu Ser Phe Phe Glu Lys Met Asp Arg Asn Lys Asp Gly
 210 215 220

Val	Val	Thr	Ile	Glu	Glu	Phe	Ile	Glu	Ser	Cys	Gln	Gln	Asp	Glu	Asn
235					230					235					240

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
245 250

```

0210> 23
0211> 1859
0212> DNA
0213> Homo sapiens

```

```

(220>
(221> CDS
(222> (207) .. (866)

```

```

04000> 25
ctcaccctgct gctcagtggtt cctctctctg ctccaggacc tccgggtaga cctcagaccc 60
tgggcacatt cccagactca gctcagccc ggaacttccc agccccgaca gcacagtagg 120
tcgcacagggg ggcgcgtgtg aggcacctat ccgggcacac cgggcgcccc tcccacggcc 180
tggggggggag cggggcgccg gggggc atg cgg ggc cag ggc cgc aag gag agt 233
Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5

```

ttg tcc gat tcc cga gac ctg gac ggc tcc tac gac gag ctg acg gac 281
 leu ser asp ser arg asp leu asp gly ser tyr asp gln leu thr asp
 10 15 20 25

[illegible]

ggt ctg gag cag ctg cag gag caa acc aaa ttc acg cgc aag gag ttg 377
Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu
45 50 55

Cag gtc ctg tac cgg gcc ttc aaq aac gaa tgt ccg agc gga att gtc 421
Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
60 80 100

car gag gag aac ttc aag gag att tac tcc sag ttc ttt tct caa gga 473
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 75 80 85

gag tgc agc acg tat gac act ttt cta ttg aat gag ttc tac att aac 90
Asp Ser Ser Thr Tyr Ala Thr Glu Leu Phe Asn Ala Phe Asp Thr Asn
 95 100 105

[illegible]

tat gac ctt aac aag gac ggc tgc atc acc aag gag gaa atg ctt gac 665
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 140 145 150

atc atg aag tcc atc tat gac atg atg ggc aag tac acg tac cct gca 713
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 155 160 165

ctc cgg gag gag gcc cca agg gaa cac gtg gag agc ttr ttc gag aag 761
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 170 175 180 185

atg gac aga aac aag gat ggt gtg gtg acc att gag gaa ttc att gag 809
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 190 195 200

tct tgt caa aag gat gag aac atc atg agg tcc atg gag ctc ttt gac 857
 Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp
 205 210 215

aat gtc atc tagccccag gagagggggg cagtgtttcc tgggggggacc 906
 Asn Val Ile
 220

atgctctaac cctagtcacg ggggaacctca cctttctctt ccaggtctca tctctactct 966
 acgctctcct ggggggtgga gggatccaag agcttgggga tttagtagtc cagatctctg 1026
 gagctgaagg ggcacagagag tgggcagagt gcatctcggg ggtgtttccc aactccacc 1086
 agctctcacc ccttctctgc ctgacaccca gtgttgagag tgcctctctt gtaggaattg 1146
 agcgggttccc cactctctac cctactctag aaacacacta gagcgatgtc tctgctatg 1206
 gtgcttcccc catccttgac ctacataaaca tttcccttaa gactcccttc tcagagagaa 1266
 tgcctccttc ttggcaactgg ctggctcttc agaccagcca ttgagagccc tgtgggaggg 1326
 ggacaagaat gtatagggag aaatcttggg cctgagtcac tggataggtc ctaggaggtg 1386
 ggtgggggtt agaatagaag ggcttggaac gattatgatt gctcaggeat accaggttat 1446
 agctccaagt tccacaggtc tctacacaca ggcctcaca atataagtt ccaggctttt 1506
 cagaagacct tctctctta gaaatgcacc aaaaattttt caaacctttt tgggtttttt 1566
 tggagagcct ggggcacgat atctggtctc tctctggcat tcttctctct ccttctcttc 1626
 tgcctgtgtt ggtggtggtt gtggtggggg aatgtggatg ggggatgttc tgggtgagc 1686
 ctgcacaaat tctctctac cctctctgt ctactctctt gtcttgagg ctatgactt 1746

<213> Homo sapiens

<400> 24

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
1 5 10 15

Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Asp Asp Glu Phe Glu
20 25 30

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
35 40 45

Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
50 55 60

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
165 170 175

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
180 185 190

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
210 215 220

<210> 18

<211> 2191

<212> DNA

<213> Simian sp.

<220>

<221> CDS

Met	Arg	Gly	Gln	Gly	Arg	Lys	Glu	Ser	Leu	Ser	Asp	Ser	
1				5					10				
cga gac ctg gac gga tcc tac gac cag ctc acg gac agc gtg gag gat	219												
Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Glu Asp													
15 20 25													
gaa ttt gaa ttg tcc acc gtg tgt cac cgg cct gag ggt ctg gag cag	267												
Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln													
30 35 40 45													
ctg cag gag caa acc aaa ttc acg cgg aag gag ttg cag gtc ctg tac	315												
Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr													
50 55 60													
cgg ggc ttc aag aac gaa tgt cgg agc gga att gtc aat gag gag aac	363												
Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn													
65 70 75													
ttc aag caa att tac tcc cac ttc ttt cct caa gga gac tcc agc acc	411												
Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr													
80 85 90													
tat gcc act ttt ctc ttc aat gcc ttt gac acc aac cat gat ggc tgg	459												
Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser													
95 100 105													
gtc agt ttt gag gac ttt gtg ggt ggt ttg tcc gtg att ctt cgg gga	507												
Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly													
110 115 120 125													
act gta gat gac agg ctt aat tgg gcc ttc aac ttg tat gac ctc aac	555												
Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn													
130 135 140													
aag gac ggc tgc atc acc aag gag gaa atg ctt gac atc atg aag tcc	603												
Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser													
145 150 155													
atc tat gac atg atg ggc aag tac aca tac cct gca ctc cgg gag gag	651												
Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu													
160 165 170													
gac cca agg gaa cat gtg gag aac ttc ttc cag aag atg gac aga aac	699												
Ala Pro Arg Glu His Val Gln Asn Phe Phe Gln Lys Met Asp Arg Asn													
175 180 185													
aag gat ggc gtg gtg acc att gag gaa ttc att gag tct tgt caa aag	747												
Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys													
190 195 200 205													
gat gag aac atc atg agg tcc atg cag ctc ttt gac aat gtc atc	792												
Asp Glu Asn Ile Met Arg Ser Met Thr Thr Phe Thr Thr Thr Thr													

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
65 70 75 80

Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
85 90 95

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
100 105 110

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
115 120 125

Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
130 135 140

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
145 150 155 160

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
165 170 175

Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
180 185 190

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
195 200 205

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
210 215 220

00100: 27

00110: 2057

00120: DNA

00130: Simian sp.

00200:

00210: CDS

00220: (208)..(963)

04000: 27

tgctgcccaa ggtctctgct cctgccccag gaetctgagg tgggccctaa aaccacagcc 60

tctctaaaga aaagccttgc cagccctctc tctcgcctcc caactccagg agttcgttcc 120

gcagccaggg ggcgttcttc cagccctctc tctcgcctcc caactccagg agttcgttcc 180

ccaggcggga gggggggccc gggggccc atg cgg ggc caa ggc aga aag gag agt 240

Met Arg Gly Gln Gly Arg Lys Glu Ser
1 5

ttg ttc caa ttc cga gat atg gac ggc ttc tat gac cag att aag ggc 300

Leu Ser Glu Ser Arg Asn Leu Ser Glu Cys Thr Thr Thr Thr Thr Thr Thr

00100: 27
00110: 2057
00120: DNA
00130: Simian sp.

00200:

00210: CDS

00220: (208)..(963)

Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
45 50 55
agc gta gag gat gag ttt gaa tta tcc acg gtg tgt cac cga cct gag 426
Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
60 65 70
ggc ctg gaa caa ctg cag gaa cag acc aag ttc aca cgc aga gag ctg 474
Gly Leu Glu Gln Leu Gln Glu Thr Lys Phe Thr Arg Arg Glu Leu
75 80 85
cag gtc ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc 522
Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
90 95 100 105
aac gag gag aac ttc aag cag att tat tct cag ttc ttc ccc caa gga 570
Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
110 115 120
gac tcc agc aac tat ggt act ttt ctg ttc aat gcc ttt gac acc aac 618
Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
125 130 135
cac gat ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg 666
His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
140 145 150
att ctg cgg ggg acc ata gat gat aga ctg agc tgg gct ttc aac tta 714
Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu
155 160 165
tat gac ctg aac aag gac ggc tgt atc aca aag gag gaa atg ctg gac 762
Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
170 175 180 185
att atg aag tcc atc tat gac atg atg ggc aag tac aca tac cct gcc 810
Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
190 195 200
ctc cgg gag gag gcc cca aga gaa cac gtg gag agc ttc ttc cag aag 858
Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
205 210 215
atg gac agg aac aag gac ggt ctg gtg acc atc gag gaa ttc atc gag 906
Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Ile Ile Glu
220 225 230
tct tgt caa cag gac gag aac atc atg agg tcc atg cag ctg tca ccc 954
Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
235 240 245
att ctg aac tgaatcag tgcaggagc aacccaggtg tagggaccaa 1008
Leu Leu Asn

tggggacaaag aaagcagaaa agtcttgga ccagagccagt ggttaggtcc taggaattgg 1243
 ctggagtggg ggcacagaaag cctgggcaga tgatgagag ccagctgggc tgcactgca 1303
 ggttcggggg cctacagccc tgggtcagca gagtatgagt tccagactt tccagaaggt 1363
 ctttagcaat gtccagaaa ttcacccgtac actttctcagt gtcttaggag ggcgcgggat 1423
 ccagatgtct ggttcctccc tgaatcctct cctccttct tgcctgtatg gtgggagtgg 1483
 tggccagggg aagatgagtg gtgtcccgga tgatgcctgt caaggtccca cctccctcc 1543
 ggctgttctc atgacagctg ttgtgttctc catgacccct atctagatgt agaggcatgg 1603
 agtgagtcag ggatttcctg aacttgagtt ttaaccctcc tcttagtggc tgccttaggg 1663
 gaatgggaag aaccacgtgt gggggcacc attagaatct ttgcgcgggt cctcacaatg 1723
 ccttagggtc ccttagggta ccgcctcct ctgtttagtc taccagaga tgcctctgag 1783
 ctcactaga ggttagggac ggtaggtcc aggtccacc tctccaggtc agcacctgc 1843
 catgtgtgtg ctctcatta acaaacctgc tctctctc ctgcgcctct tctcagtcag 1903
 ccagcgtctg aggggaaggg cctcccgttt ccccatcct cagacatggt tgaactgctt 1963
 gcattttggg ctctctctc tttttgtaa aataagacat cagatccaat aaaacacacg 2023
 gctatgcaca aaaaaaaaaa aaaaaaaaaa aaaa 2057

(210): 28
 (211): 282
 (212): PRT
 (213): Simian sp.

(400): 28
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Arg Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

Leu Lys Phe Gln Leu Leu Leu Leu Leu Lys Arg Ser Ser Asn Tyr Ala Thr
 85 90 95 100 105 110 115 120 125 130 135 140 145 150

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
132 133 140

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 150 155 160

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 170 175

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 200 205

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
210 215 220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
235 239 243 247

Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
 245 250

- 0101: 29
- 0111: 1904
- 0121: DNA
- 0131: Rattus sp.

- 0120:
- 0121: CDS
- 0122: (1)..(675)

84900- 29
 ang aac cac tgc cct cgc agg tgc cgg agc ccg ttg ggg cag gca gct 48
 Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
 1 5 10 15

cga tct ctc tac cag ttg gta act ggg tgg ctg tgg cca gac agc gta 96
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30

Gag Gai Gaa Iit eae tte toe asg ety tyt oao aga oot gao ngo ety 144
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Gly Gly Ile
 35 40 45

gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg cag gtc 192
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
50 55 60

tgg tac gga gag ttg aag aac gaa tgc ccc agt ggg att gta aac gag 840
 tgg tgg acc atp ttc ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt

1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993

100					105					110						
ggc	tct	gtc	agt	ttt	gag	gac	ttt	gtg	gct	ggc	ttg	tgc	gtg	att	ctt	384
Gly	Ser	Val	Ser	Phe	Glu	Asp	Phe	Val	Ala	Gly	Leu	Ser	Val	Ile	Leu	
		115					120					125				
egg	ggg	acc	ata	gat	gat	aga	ctg	agg	tgg	gct	ttc	aac	tta	tat	gac	432
Arg	Gly	Thr	Ile	Asp	Asp	Arg	Leu	Ser	Trp	Ala	Phe	Asn	Leu	Tyr	Asp	
		130					135					140				
ctc	aac	aag	gac	ggc	tgt	atc	aca	aag	gag	gaa	atg	ctt	gac	att	atg	480
Leu	Asn	Lys	Asp	Gly	Cys	Ile	Thr	Lys	Glu	Glu	Met	Leu	Asp	Ile	Met	
		145					150					155				
aag	tcc	atc	tat	gac	atg	atg	ggc	aag	tac	aca	tac	cct	gac	ctc	egg	528
Lys	Ser	Ile	Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Ala	Leu	Arg	
				165					170					175		
gag	gag	gac	cca	aga	gaa	cac	gtg	gag	agg	ttc	ttc	cag	aag	atg	gac	576
Glu	Glu	Ala	Pro	Arg	Gln	His	Val	Glu	Ser	Phe	Phe	Gln	Lys	Met	Asp	
			180						185					190		
agg	aac	aag	gac	ggc	gtg	gtg	acc	atc	gag	gaa	ttc	atc	gag	tct	tgt	624
Arg	Asn	Lys	Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe	Ile	Glu	Ser	Cys	
			195				200					205				
caa	cag	gac	gag	aac	atc	atg	agg	tcc	atg	cag	ctc	ttc	gat	aat	gtc	672
Gln	Gln	Asp	Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu	Phe	Asp	Asn	Val	
		210					215					220				
atc	tagctcccca	gggagagggg	ttagtgtgtc	ctagggtgac	cagggtgtag											725
Ile																
ttctagtcca	gacgaacctc	acctctctct	tccaggcctg	tcttcattct	acctgtacct											785
tgggggctgt	agggattcaa	tatcctgggg	cttcagtagt	ccagatccct	gagctaagtc											845
acaaaagtag	gcaagagtag	gcaagctaaa	tctgggggct	tcccaacccc	cgacagctct											905
caccctctct	caactgatac	ctagtgtgtg	ggacacccct	ggtgtaggga	ccaagtgggt											965
ctccctctct	tagtccact	ctagaaacca	cattagacag	aaggtctct	gtatagggtg											1025
tttccctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct											1085
gtccatgtcc	ccagctggct	tctcagccta	gcctttgagg	gcctgtgggg	gaggggggga											1145
caagaaagca	gaaaagtctt	ggccccgagg	tagtggttag	gtctaggtaa	ttgggtggag											1205
tggatgtag	aaaatgtgtt	cagatgatga	gagataggt	aggtgtgac	tctatgtct											1265
tttccctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct											1325
tttccctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct											1385
tttccctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct									</		

ttcctcaccac tgcctataggg tccctataggg taaccgctcc ctatgttttag tctaccacaga 1625
 gatgtctctg agctcaccct gagggtaggg acggttaggt ccaggtccaa cctctccagg 1685
 ccagcaccct gcctatgtgc tgcctctcat taacaaacct gcttgtctcc tctgagccac 1745
 ttctcagtc agccaggggtc tgagggggaag ggctccctgt tccccatcc gtcagacatg 1805
 gttgactgct ttgcattttg ggcctcttcta tctattttgt aaaataagac atcagatcca 1865
 ataaacaca cggctatgca caaaaaaaaa aaaaaaaaaa 1904

#210 - 30
 #211 - 225
 #212 - PET
 #213 - Rattus sp.

#400 - 30
 Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
 1 5 10 15
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 35 40 45
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 50 55 60
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 65 70 75 80
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 85 90 95
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 100 105 110
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 115 120 125
 Arg Gly Thr Ile Asp Asp Arg Leu Ser Tyr Ala Phe Asn Leu Tyr Asp
 130 135 140
 Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
 145 150 155 160
 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
 165 170 175

#210 - 30
 #211 - 225
 #212 - PET
 #213 - Rattus sp.

#400 - 30
 Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
 1 5 10 15
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 35 40 45
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 50 55 60
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 65 70 75 80
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 85 90 95
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 100 105 110
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 115 120 125
 Arg Gly Thr Ile Asp Asp Arg Leu Ser Tyr Ala Phe Asn Leu Tyr Asp
 130 135 140
 Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
 145 150 155 160
 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
 165 170 175

Ile
225

<210> 31
<211> 2841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(768)

<100> 31
atg cag ccg gct aag gaa gtg aca aag gcg tcg gac ggc agc ctc ctg 48
Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
1 5 10 15
ggg gac ctc ggg cac aca cca ctt agc aag aag gag ggt atc aag tgg 96
Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
20 25 30
cag agg ccg agg ctc agc cgc cag gct ttg atg aga tgc tgc ctg gtc 144
Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
35 40 45
aag tgg atc ctg tcc agc aca gcc cca cag ggc tca gat agc agc gac 192
Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60
agt gag ctg gag ctg tcc aag gtg cgc cac cag cca gag ggg ctg gac 240
Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
65 70 75 80
cag ctg cag gcc cag acc aag ttc acc aag aag gag ctg cag tct ctc 288
Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95
tac agg ggc ttt aag aat gag tgt ccc acg ggc ctg gtg gac gaa gac 336
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110
acc ttc aaa ctc att tac gcc cag ttc ttc cct cag gaa gat gcc acc 384
Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125
acc tat gca cac ttc ctc ttc aac gcc ttt gat gcc gac ggg aac ggg 432
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
130 135 140
tgc atc cac ttt gag gac ttt gag gtt ggc ctc tcc atc atg ctg agg 480
Ala Ile His Phe Gln Asn Phe Val Val Thr Leu Ala Thr Thr Thr Thr

180 185 190

100 atc tat gac atg atg ggc ggc cac acc tac ccc atc ctg cgg gag 624
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205

gac gag ccc gag gag cac gtc gag agg ttc ttc gag aaa atg gac cgg 672
 Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
 210 215 220

aac cag gat ggg gta gtg acc att gaa gag ttc ctg gag gcc tgt cag 720
 Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
 225 230 235 240

aag gat gag aac atc atg agc tcc atg cag ctg ttc gag aat gtc atc 768
 Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250 255

taggacacgt ccaaaaggagt gcacggccac agccacctcc aaccccaaga aacctccatc 824
 ctgcacaggag cagcctccaa gaaactttta aaaaatagat ttgcacaaaag tgaacagatt 888
 gctacacaca cacacacaca cacacacaca cacacacaca cacagccatt catctggggt 948
 ggcagagggg acagagttca gggagggggt gagtctgggt aggggcccag tccaggagcc 1008
 ccagccagcc ctccccaggg cagcgaggcg aggetgcctc tgggtgagtg gctgacagag 1068
 caggtctgca ggcacccagc tgcctgatgt caccaagaag ggcctcagat gccctgcag 1128
 ggcagggctc aatctccggg gtgagccac ctgctccgt tctccattct gctttcttgc 1188
 cacacagtg ggcggcccca ggcctccctg gtctccctcc cgtagccact ctctgccac 1248
 tacctatgt cttagaaaag cctccacctc aggcacccag agggaccagc tggggggcag 1308
 gggggagagg gggtaatgga ggcbaagcct gcagctttct ggaaattctt cctgggggt 1368
 ccaggatcc cctgctaact cactgacctg gaagagctgg gtaccaggcc acccactgtg 1428
 ggcbaagcct gagtggcgag gggccactgg gccccattct cctccatgg caggaaggcg 1488
 ggggatttca agtttaggga tgggtctg gtggagaac tgaaggccact ctctgcagc 1548
 tccaggtat ggtagagc tctcttctc aggtcttg ttagggga ctctggggg 1608
 tggggtgta cacacctcc agcacagaact gtccctcca aggtctctt aggtccggg 1668
 aggaacgtg ttcagagact ggcagccagg gacccgggg cagagctcag aggagtctgg 1728
 gaagggctt ctccctctc tctctgtat ccccttcca tggccaca ca gttgtgta 1788
 ggcctctc tgaagcatt gtcctctc ctctcttg ggcctctc tgaagcatt gtcctctc

gaatgacagc ccaaaagctgg agccaatggt gagggctgag agggctgtgg ctgggtgggc 2148
 agcagaaaaa cccaggagga gagagatgct gctcccgctt gattggggcc tcaccagaa 2208
 ggaacccgggt cccaggccgc atggcccttc caggaacatt cccacataat acattccatc 2268
 acagccagcc cagctccact cagggtctgg ccggggagtc cccgtgtgac ccaagaggct 2328
 agccccaggg tgagccaggg cctcagagga aaggcagtat ggccgagggc atggggggcc 2388
 ctgggcattc acacacagcc tggcctcccc tggggagctg catggaagcc tggctccagg 2448
 tccagggtg actgggggac tatgctccca ggagggcacc agctttccct ggctccagga 2508
 tctttccct cccctccacc gctgcccagc cctccagctt ggtgtccctc tgcctctaac 2568
 gccaaaggct caggagagca tcaccaccac accctggccg gcttggcctt tggggccaga 2628
 ctgggtgcac agcccaacca agaggggtct gctccccag ctgggaccca gacccggccc 2688
 atgtctgcat ggcagaagcg tctcccttgg ccaaggccctg ggaggggtgt tctgtttctc 2748
 agcatccact aatattcagt cctgttatatt ttaataaaat aaacttgaca aaggaaaaaa 2808
 aaaaaaaaaa aattccctgg gcgcggttct cca 2841

<210> 32

<211> 256

<212> PRT

<213> Homo sapiens

<400> 32

Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
 1 5 10 15

Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
 20 25 30

Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
 35 40 45

Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
 50 55 60

Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
 65 70 75 80

Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
 85 90 95

Tyr Arg Gly Phe Lys Arg Gln Thr Lys Thr Thr Thr Thr Thr Thr Thr

Thr Tyr Ala His His Leu His Asn Ala Ile Arg Ala Arg Gly Asn Gly
 100 105 110

1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398</
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	--------

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
165 170 175

Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
181 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
195 200 205

Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
216 215 220

Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
233 230 235 240

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

0010 - 33
 0011 - 442
 0012 - DNA
 0013 - *Rattus* sp.

- 02.10 •
- 02.11 • CDS
- 02.12 • (1) .. (32)

5400 + 35
 TTT TGG GAC TTT GTG GTT GGG CTC TCC ATC CTG CTT CGA GGG ACC GTC 48
 Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
 : 5 10 15

Cat. gag aag ctc aag tgg gcc ttc aat ctc tac gac atc aac aag gac 96
 His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
 20 25 30

ggg tac atc acc aaa gag gag atg ctg gcc atc atg aag tcc atc tac 144
Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
35 40 45

100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120
 Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
 50 55 60

ctg gag cat gtg gag agg ttc ttc cag aaa atg gac agg aac cag gat 240
Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
68 72 76 80

[illegible]

gag tta tcc aac gtg cgc cat cag cca gag ggc ttg gac cag cta caa 297
Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp Gln Leu Gln
70 75 80

ggt cag acc aag ttc acc aag aag gag ctg cag tcc ctt tac cga ggc 345
Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu Tyr Arg Gly
85 90 95

ttc aag aat gag tgt ccc aca ggc ctg gtg gat gaa gac acc ttc aaa 393
Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp Thr Phe Lys
100 105 110 115

ctc att tat tcc cag ttc ttc cct cag gga gat gcc acc acc tat gaa 441
Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr Thr Tyr Ala
120 125 130

cac ttc ctc ttc aat gcc ttt gat ggt gat ggg aac ggg gcc atc cac 489
His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly Ala Ile His
135 140 145

ttt gag gac ttt gtg gtt ggg ctc tcc atc ctg ctt cga ggg aac gtc 537
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
150 155 160

cat gag aag ctc aag tgg gcc ttc aat ctc tat gac att aac aag gat 585
His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
165 170 175

ggt tgc atc acc aag gag gag atg ctg gcc atc atg aag tcc atc tac 633
Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
180 185 190 195

gac atg arg ggc cgc cac acc tac ccc atc ctg cgg gag gat gaa ccc 681
Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
200 205 210

ctg gag cat gtg gag agg ttc ttt cag aaa atg gac agg aac cag gat 729
Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
215 220 225

gga gtg gtg acc atc gat gaa ttt ctg gag act ttt cag aag gat gag 777
Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
230 235 240

acc atc atc aac ttc atg cag ctg ttt gaa aac gtc atc taggagc 801
Asn Ile Met Asn Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

gggaggggac cccagtggtc attgottctc aacccagaga agcctcaatc ctgacaggag 886

aagcctctat gagaaacatt ttctaatat atttgcacaaa agtgagcagc ttactctaaa 946

ggagatcaaa ctattccctg cctataggac catgctctta ggaagctccc agaaactcna 1246
aggggacaaa gagggagag gtctatagga agaaatggtt ttggaagctg ggattgagc 1306
cttatgctaa tgatccctg gggctctgga acccgagtgc caggctacct actatgctgt 1366
gagcttagat agtgaggggc cattggacta agacctcttg taagagtggg gcaggattga 1426
ggtttttgga gaaactgagg aaacaatttg tccataccac tgggtgaaga ctgctggcca 1486
gtgggaatgt ggtctgtgga gatttcccaa cttccagcac caggatggcc tctccaaggt 1546
cctctttgat tccctgggga gatccctgg ctcatagact gacaaccagg gaactgggct 1606
gaaatgggag gtctggtagg gggcatcccc ctccttttcc ctggccactt gccacccagt 1666
tccttaaac acgtggatgg ccacacctct gtggtctgcc ttgaacagac tcctcccgac 1726
caagacaaaa aagcacaaac tcttagcagc tcaggccaag cccacaaggg aaggcctggg 1786
tccctgcagc cctgatccag tggccgagga agacgtccag acatccatcc tgtacctgg 1846
agccttgggg gtctcacagc cctttccag cccagctcgc caacattcta aagcacaaac 1906
ctggcgatcc tcttctcttg ggtctgcccc tggggattga aggcacctgt taaccttaag 1966
ctggagctag cctcgagggc tggggaacct tgaccaggea acaggtcagc agacctcag 2026
gaggagagag agctgttccct gcttccccag gcttcgcccc gaaggaaacag tgtcccaaga 2086
agcatgttct ctggagggaac atccccacaa aagtacattc catcatctga agcccggtct 2146
ctgctcaggc ctgctctga aagtccacgt gtgttcccca gaaggccagc cccaagataa 2206
gggaggtcct tagaggaagg acagggtgac aacaccccta tacacaggtg gacccccct 2266
ctgaggaactg tactgacccc atctccatcc tgaccggggc ctctctttac ccgatctaca 2326
gaccaccagt tctccctggt ccagggaacc cctgtcccc agtctgactc tcccatcga 2386
ggtccctgtc ttgtgaaaag ccaaggccac gggaaaaggc caccactcta acctgctgca 2446
tccttagcc cctgctgca cgcctaacct gtaggggtct gtccttttg cagggaaca 2506
tctggagc ctctccac cccaggaagg tctctctg gtagactg gagggtgt 2566
ctctgtctca ggcctccca atattcagtc ctatatattt taataaaaga aacttgacaa 2626
agggaaaaaa aaaaaaaa 2644

* 210 - 36
* 211 - 256

Mon. Tue. Wed. Thu. Fri. Sat. Sun. Mon. Tue. Wed. Thu. Fri. Sat. Sun.

Gly Asp Pro Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp
 20 25 30
 Gln Arg Pro Arg Phe Thr Arg Gln Ala Leu Met Arg Cys Cys Leu Ile
 35 40 45
 Lys Trp Ile Leu Ser Ser Ala Ala Pro Gln Gly Ser Asp Ser Ser Asp
 50 55 60
 Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
 65 70 75 80
 Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
 85 90 95
 Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
 100 105 110
 Thr Phe Lys Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr
 115 120 125
 Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
 130 135 140
 Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
 145 150 155 160
 Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
 165 170 175
 Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
 180 185 190
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205
 Asp Ala Pro Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg
 210 215 220
 Asn Gln Asp Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln
 225 230 235 240
 Lys Asp Glu Asn Ile Met Asn Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250 255

<210> 27
 <211> 531
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<230> 1000
 <231> 1000
 <232> 1000
 <233> 1000
 <234> 1000

```

cac gag gtg gaa agc att tac gct cag ctg gag gag gcc agc tct aca    48
His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
   1             5             10             15

ggc ggt ttc ctg tac gct cag aac agc acc aag cgc agc att aaa gag    96
Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
             20             25             30

cgg ctc atg aag ctc ttg ccc tgc tca gct gcc aaa acg tcg tct cct    144
Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
             35             40             45

gct att caa aac agc gtg gaa gat gaa ctg gag atg gcc acc gtc agg    192
Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg
             50             55             60

cat cgg ccc gaa gcc ctt gag ctt ctg gaa gcc cag agc aaa ttt acc    240
His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr
             65             70             75             80

aag aaa gag ctt cag atc ctt tac aga gga ttt aag aac gta aga act    288
Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr
             85             90             95

ctc ttt ttg act tta cct tca cac aat tcc cag agg agc att gag aaa    336
Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
             100            105            110

cgagaggaaa aggggggaaaa tatcccatc tatgagaagc cccatcatat gtatatttca 396

tactgatcct tccagatag gaatataatc agtatctgtg gactttgaat ctctgtggca 456

caccatgct ggcatactgt aattgcccac taaacaaaana gtttttgaga aaaaaaaaaa 516

aaaaaaaaaa aaaaaa                                                    531

```

<210> 38
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 38
His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
   1             5             10             15

Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
             20             25             30

Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
             35             40             45

```

Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Thr Val Arg Thr

Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr

Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
 100 105 110

<210> 39
 <211> 2176
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2)..(124)

<400> 39
 1 gaa agg ttc ttc gag aaa atg gac cgg aac cag gat ggg gta gtg acc 40
 Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
 1 5 10 15

att gaa gag ttc ctg gag gcc tgt cag aag gat gag aac atc atg agc 47
 Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
 20 25 30

tcc atg cag ctg ttt gag aat gtc atc taggacacgt ccaaaggagt 144
 Ser Met Gln Leu Phe Glu Asn Val Ile
 35 40

gcattggccac aggcacctcc acccccaga aacctccatc ctggccaggag cagcctccaa 104
 gaaactttta aaaaatagat ttgaaaaag tgaacagatt gctacacaca cacacacaca 164
 cacacacaca cacacacaca cacagcatt catctggggt ggcagagggg acagagtcca 224
 gggagggggt gagtctgggt aggggcagag tccaggagcc ccagccagcc ctccccaggc 284
 cagcgaggcg aggtctgcctc tgggtgagtg gctgacagag caggtctgca ggcaccagc 344
 tgctggatgt caccagaag ggctctgagt gccctgcag gggagggctc aatctccggt 404
 gtgagccac ctgctccgt tctccattct gctttcttgc cacacagtgg gccggcccca 464
 ggctcccttg gtctctccc cgtagccact ctctgccac tacctatgct tctagaaagc 524
 ccttacctc aggaaccag agggaccagc tggggggcag gggggagagg gggtaattga 584
 tgcacacac gaagcttctt ggaattctt cctgggggt cccaggatc ctctctctc 644
 cactgacctg gaagagctgg gtaccaggcc acccactgtg gggcaagcct gagtggtgag 704
 gggccactgg gccccattct cctccatgg caggaaggcg ggggatttca agtttaggga 764
 tgggtctgtg gtggagaatc ttagggcact ctctgacagc tccacaggtt gggatjagc 824
 tctcttggc cagctctgtt tctctctt tctctctt tctctctt tctctctt 884

gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 944
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 1004
 gggggggggg gggggggggg gggggggggg gggggggggg gggggggggg 1064

cctagtggga gccagcaca ctgtttctcg gaggccagga cctcctgctg gctgaggctt 1284
 gggcccagta gcccacatat ggtggccctg gggaagagga cttggggggtc tctctctgtg 1344
 ctgggatcag tggggcccca aagcccagcc cggtcgacca acattcaaaa gcacaaaacc 1404
 tgggjaetct gcttggtgtt cccctccatc tggggatgga gaatgcagc ccaagctgg 1464
 agccatgggt gagggtcgag agggctgttg ctgggtggtc agcagaaaa cccaggagga 1524
 gagatctgt gctcccgctt gattgggggc tcaccagaa ggaaccgggt cccaggccgc 1584
 atggccctc caggaacatt ccacataat acattccatc acagccagcc cagctccact 1644
 caggcttggc cgggggagtc cccgtgtgcc ccaagaggtt agcccagggt ttagcagggc 1704
 cctcagagga aaggcagtat ggcggaggcc atggggggcc ctgggcattc acacacagcc 1764
 tggctccccc tgggagctg catggagccc tggctccagg ctccaggctg actgggggccc 1824
 tatgtctcca ggagggcata agctttccct ggctcaggga tcttctccct cccctccccc 1884
 gctgcacagc cctccagctt ggtgtccatc tgcctctaag gccaggcct caggagagca 1944
 tcacacccac acccctgcgc gcttgggctt tggggccaga ctggctgcac agcccaacca 2004
 ggaggggtct gctcccaag ctgggacaca gacgggcgc atgtctgcac gccagaagcg 2064
 tctcccttgg ccacggcctg ggagggtgtt tctgtttct agcatccact aatattcagt 2124
 cctgtatatt ttaataaaat aaacttgaca aaggaaaaaa aaaaaaaaaa aa 2176

<210> 40
 <211> 41
 <212> PRT
 <213> Homo sapiens

<400> 40
 Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
 1 5 10 15
 Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
 20 25 30 35
 Ser Met Gln Leu Phe Glu Asn Val Ile
 35 40

<210> 41
 <211> 2087
 <212> DNA

<4> 41

tcttataaaga aaagctttgc cagcccccatac tccggggccc caaccccaga aggtatctgc 120

ggcgccaggg ggagctgtgt gagcgcccta ttctggccac cggggggccc ctcccaaggg 180

ccaggcgggga gggggggccc gggggccc atg cgg ggc caa ggc aga aag gag agt 234

Met Arg Gly Gln Gly Arg Lys Glu Ser

1

5

ttg tcc gaa tcc cga gat ctg gac ggc tcc tat gac cag ctt acg ggc 282

Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly

10

15

20

25

cac cct cca ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc ctc aag 330

His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys

30

35

40

ctg ctg ccg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt gaa aac 378

Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn

45

50

55

agc gta gag gat gag ttt gaa tta tcc aag gta tgt cac cga cct gag 426

Ser Val Glu Asp Glu Phe Gln Leu Ser Thr Val Cys His Arg Pro Glu

60

65

70

ggc ctg gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg 474

Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu

75

80

85

cag gtc ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc 522

Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val

90

95

100

105

aac gag gag aac ttc aag cag att tat tct cag ttc ttc ccc caa gga 570

Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly

110

115

120

gac tcc agc aac tat gct act ttc ctc ttc aat gcc ttt gac acc aac 618

Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn

125

130

135

cac gat ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg 666

His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val

140

145

150

att ctt cga ggg acc ata gat gat aga cta gat tgg act ttc aat tta 714

Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu

155

160

165

tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac 762

Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp

170

175

180

185

ctc att att att att att att att att att att att att att att att att 814

Leu Arg Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu

190

195

200

atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc atc gag 905
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 220 225 230
 tct tgt caa cag gac gag aac atc atg agg tcc atg cag ctc tca ccc 906
 Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
 235 240 245
 ctt ctc aac tgatacctag tgctgaggac acccctggtg tagggaccaa 1003
 Leu Leu Asn
 250
 gtgggtctctcc acctttctagt cccactctag aaaccacatt agacagaagg tctcctgcta 1003
 tgggtgcttcc cccatcccta atctcttaga tttctctcaa gactcccttc tcagagaaca 1103
 cgtctgtctcc atgtcccccag ctgggtctctc agcctagcct ttgaggggccc tgtggggagg 1103
 cgggggacaag aaagcagaaa agtcttgggc ccgagccagt ggttaggtcc taggaattgg 1243
 ctggagtggg ggcacagaaag cctgggcaga tgatgagagc ccagctgggc tgtcactgca 1303
 ggttcggggg cctacagccc tgggtcagca gagtatgagt tccagactt tccagaaggt 1363
 ccttagcaat gtcccagaaa ttcacogtac aactctcagt gtcttaggag ggcgcgggat 1423
 ccagatgtct ggttcctccc tgaatctct cctcctctt tgcctgtatg gtgggagtgg 1483
 tggccagggg aagatgagtg gtgtcccgga tgatgctgt caaggctccc cctccctccc 1543
 ggctgtctct atgacagctg ttgggtctct cagacccct atctagatgt agaggcatgg 1603
 agtgagtccg ggatttcccg aacttgagtt ttaaccactc tctagtggc tgccttaggg 1663
 gaatgggaag aaccacagtgt gggggcacc cttagaatct ttgcocggct cctcacaatg 1723
 ccttagggtc ccttagggta ccgcctccct ctgttttagtc taaccagaga tgcctctgag 1783
 ctacactaga ggytagggac ggtaggctcc aggtccaacc tctccaggtc agcaccctgc 1843
 catgtctctg ctctcatta acaaaactgc ttgtctcttc ctgcgcctct tctcagtcag 1903
 ccagggtctg aggggaaggg cctcccgctt cccatccgt cagacatgtt tgaactgctt 1963
 gcatctggg cttctctct tctttctaa actaagat cagatcact aacacacag 2023
 gctatgcaca aaaaaaaaaa aaaaaaaaaa aaaa 2057

<210> 42

<211> 252

<212> FRT

<213> Rattus sp.

Acc Gly Ala Gly Asp His Ile Thr Gly His Pro Pro Gly Ile Pro Ile
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
35 40 45
Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
50 55 60
Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
65 70 75 80
Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe
85 90 95
Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
100 105 110
Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
115 120 125
Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
130 135 140
Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 150 155 160
Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 170 175
Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
180 185 190
Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 200 205
Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
210 215 220
Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
225 230 235 240
Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
245 250

<210> 43

<211> 26

<212> FRT

<213> Artificial Sequence

<220>

<221> misc_feature

<222> 2,5,6,9,17,25,26

<223> Met, Ile, Leu, Val or Met

<224>

<225> Description of Artificial Sequence: *in vitro*

<400> 43

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Lys Asp Gly Asp Gly Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Glu Phe Xaa Xaa Xaa Xaa
20 25

<210> 44

<211> 40

<212> DNA

<213> Rattus sp.

<400> 44

taa'acgaact cactataggg actggccatc ctgctctcag 40

<210> 45

<211> 40

<212> DNA

<213> Rattus sp.

<400> 45

attaacccctc actaaaggga cactactgtt taagctcaag 40

<210> 46

<211> 40

<212> DNA

<213> Rattus sp.

<400> 46

taa'acgaact cactataggg cacctccctt ccggtctgtc 40

<210> 47

<211> 40

<212> DNA

<213> Rattus sp.

<400> 47

attaacccctc actaaaggga gagcagcagc atggcagggt 40

<210> 48

<211> 2413

<212> DNA

<213> Simian sp.

<220>

<221> CDS

<222> (CDS)... (CDS)

... ..

... ..

aagcctgaag ttgtacgat tctgtaatta acctccctcca ctccaaaggg gtctggaggg 247
tgggatgctc tggagatcca gagg atg ttg act ctg gag tgg gag tcc gaa 291
Met Leu Thr Leu Glu Trp Glu Ser Glu
1 5
gga ctg caa aca gtg ggt att gtt gtg att ata tgt gca tct ctg aag 339
Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25
ctg ctt cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40
gat gaa ctg gag atg gcc act gtc agg cat cgg cct gag gcc ctt gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 50 55
ctt ctg gaa gcc cag agc aaa ttt acc aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70
tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
Tyr Arg Gly Phe Lys Asn Gln Cys Pro Ser Gly Val Val Asn Glu Glu
75 80 85
acc ttc aaa gag att tac tgg cag ttc ttt cca cag gga gac tct aca 579
Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
90 95 100 105
aca cat gca cat ttt ctg ttc aat ggg tct gat acg gac cac aat gga 627
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
110 115 120
gcc gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att tgg ctc cgg 675
Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
125 130 135
ggg aca gta caa gaa aaa ctc aat tgg gca ttt aat ctg tat gat ata 723
Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile
140 145 150
aat aaa gat ggc tac atc acc aaa gag gaa atg ctt gat ata atg aaa 771
Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
155 160 165
gca ata tac gac atg atg ggt aaa tgt aca tat cct gtc ctc aaa gaa 819
Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu
170 175 180 185
gat gca ctt aga caa cac gtc gaa aca ttt ttt cag aaa atg gac aaa 867
Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe Gln Lys Met Asp Lys
190 195 200 205
tat tat tat tat tat tat tat tat tat tat tat tat tat tat tat 915
Phe Asn Gln Asn Ile Met Asn Asn Met Phe Thr Leu Thr Thr Thr Thr

taacttgtoa actagatont gaatccaaca gacaaatgtg aactattota ccaccottaa 1023
agtcggagct accactttta gcatagattg ctacagcttga cactgaagca tattatgcaa 1083
acaagctttg ttttaatat aagcaatccc caaaaagattt gagtttttca gttataaatt 1143
tgcactcttt ccataatgcc actgagttca tgggatgttc taactcattt catactctgt 1203
gaatattcaa aagtaataga atctggcata tagttttatt gattccttag ccacgggatt 1263
attgaggott tncatatca gtgattttta aataccagtg tttttgtc tcatttgtat 1323
gtrattcagtc ctaggatttt gaatggtttt ctaatatact gacatctgca ttttaatttc 1383
agaaattaaa ttaattttca tgtctgaatg ctgtaattcc atttatatac ttttaagtaa 1443
caaataagat tactacaatt aaacacatag ttccagtctc tatggccttc ccttcccacc 1503
ttctattata aattaatttt atctgggtat ttttaacatt taactttta ccacagata 1563
tcagcatatg cctaattatg cctaattgaaa ctttaataagc atttaatttt ccacatata 1623
ttatagccaa ggccatata ctatatataa tcttggtatt gtttaatttt acaggctgtt 1683
ttccattgta ccacaaagtg gaagttcaag acgggcacaa acaaaaacag gatgtttaca 1743
gacatatgca aagggtcagg atatctatcc tccagtatat gttaatgctt aataacaagt 1803
aatcttaaca gcattaaagg ccaaatctgt cctctttccc ctgacttccc taacagatgt 1863
ttatattaca agccattcag ggacaaaagaa accttgacta cccactgtc tactaggaac 1923
aaacaaaacg caagcaaaat tcactttgaa agnaccagtg gttccatnac attgacaact 1983
actaccaaga ttcagtagaa aataagtgtc caacaactaa tccagatnac aatatgattt 2043
agtgcacat aaaattccaa caattcagat tatttttaat catctcagcc acaactgtaa 2103
agttgcaca ttactaaaga cacacacatc gtccctgttt tctagaaata tcacaaagac 2163
caagaggcta cagaaggagg aaattttgca ctgtcttttc aacaataat caggtatota 2223
ttctggtgta gagatagat gttagaaget gctctgtat cccactgta gaatttaag 2283
gtagacaaat acatgtaac ttaattttc catctctgt tgggtgaaa ttaattgta 2343
cattttgtat ttcaaaaaga aaaaataaaa gcaaaataaa atgttwawaa mwmwaaaaaa 2403
aaaaaaaaa 2413

2105 48

2105 48

MNI-0700 P4

[illegible]

```
<210> 50
<211> 1591
<212> DNA
<213> Simian sp.
```

```
<220>
<221> CDS
<222> (265)..(963)
```

tgggtagctc tgcagatcca gaggg atg ttg act ctg gag tgg gag tcc gaa 291
 Met Leu Thr Leu Glu Trp Glu Ser Glu
 4 5

gga ctg caa aca gtg ggt att gtt gtg att ata tgt gca tct ctg aag 339
Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25

ctg ctt cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

gat gaa atg gag atg gcc act gtc agg cat cgg cct gag gcc ctt gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 55 55

ctt ctg gaa ggc cag agc aaa ttt acg aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70

Tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val Asn Glu Glu
75 30 35

acc ttc aaa gag att tac tog sag ttc ttt cca sag gga gac tot aca 579
Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
90 35 101 195

aca tat gaa cat ttt ctg ttc aat gag ttt gat acg gac cac aat gga 627
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
110 115 120

get gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att ttg ctc cgg 675
Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
125 130 135

ggg aca gta caa gaa asa ctc aat tgg gca ttt aat ctg tat gat ata 723
Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile
140 145 150

aat aaa gat ggc tac atc act aaa gag gaa atg ctt gat ata atg aaa 771
Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Phe Met Lys
155 160 165

Ala Ala Ser Asp Arg Gly Asn Thr Ala Val Phe Ile Thr Glu Ser
Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu
170 175 180 185

gat gaa ccc aga caa cac gtc gaa aca ttt ttt cag gct gtt ttc cat 867
Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe Gln Ala Val Phe His
190 195 200

taatgcttaa taacaagtaa tcaaacagc attaaaggcc aaatctgtcc tctttccct 1223
 gaattcctta cagcatgttt atattacaag ccattcaggg acaaagaaa cttgactacc 1283
 ccactgtcta ctagggaacaa acaaacagca agcaaaaatc actttgaaa cactagtggt 1343
 tccattacat tgacaactac taccaagatt cagtagaaaa taagtgtcca acaactaact 1203
 cagattacaa tatgatttag tgcacataa attccaaca attcagatta tttttaatca 1263
 tctcagccac aactgtaaag ttgcacatt actaaagaca cacacatcgt cctgttttg 1323
 tagaatatc acaaagacca agaggctaca gaaggaggaa atttgcaact gtctttgcaa 1383
 caataaatca ggtatctatt ctgggtgtaga gataggatgt tgaaagctgc cctgctatca 1443
 ccagtgtaga aattaagagt agtacaatac atgtacactg aaatttgcca tgcgtgttt 1503
 gtgtaaactc aatgtgcaca ttttgtatct caaaaagaaa aaataaaagc aaaataaat 1563
 gttwawaamw mwaaaaaaaa aaaaaaaaa 1591

(210): 51
 (211): 233
 (212): PRT
 (213): Simian sp.

(400): 51
 Met Leu Thr Leu Glu Trp Glu Ser Glu Gly Leu Gln Thr Val Gly Ile
 1 5 10 15
 Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu
 20 25 30
 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
 35 40 45
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
 50 55 60
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
 65 70 75 80
 Cys Pro Ser Gly Val Val Asn Gln Gln Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
 115 120 125

(400): 51
 Met Leu Thr Leu Glu Trp Glu Ser Glu Gly Leu Gln Thr Val Gly Ile
 1 5 10 15
 Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu
 20 25 30
 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
 35 40 45
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
 50 55 60
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
 65 70 75 80
 Cys Pro Ser Gly Val Val Asn Gln Gln Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
 115 120 125

Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
180 185 190

Glu Thr Phe Phe Gln Ala Val Phe His Cys Ile Ile Lys Trp Lys Phe
195 200 205

Lys Thr Ala Ser Asn Lys Thr Arg Met Phe Thr Asp Ile Cys Lys Gly
210 215 220

Ser Gly Tyr Leu Ser Ser Ser Ile Cys
225 230

0010: 42

0011: 2051

0012: DNA

0013: Rattus sp.

0020

0021: CDS

0022: (85)..(1305)

0000: 42

ggtggagcta agcaactcaact ggggtgctgc cctgggtctg cagagaacaa ggaaagcttc 60

tctgcagggc tgtcagctgc caaa atg aac ggc gtg gaa ggg aac aac gag 111
Met Asn Gly Val Glu Gly Asn Asn Glu
1 5

ctc act ctc gct aac acc tgc acc tcc gcc ctt gtc ccg gaa gat ctg 159
Leu Pro Leu Ala Asn Thr Ser Thr Ser Ala Leu Val Pro Glu Asp Leu
10 15 20 25

gat ctg aag caa gac cag ccg ctc agc gag gaa act gac acg gtg cgg 207
Asp Leu Lys Gln Asp Gln Pro Leu Ser Glu Glu Thr Asp Thr Val Arg
30 35 40

gag atg gag gct gca ggt gag gcc ggt gcg gag gga gcc gcg tcc ccc 255
Glu Met Glu Ala Ala Gly Glu Ala Gly Ala Glu Gly Gly Ala Ser Pro
45 50 55

gat tcc gag cac tgc gac ccc cag ctc tgc ctc cga gtg gct gag aat 303
Asp Ser Glu His Cys Asp Pro Gln Leu Cys Leu Arg Val Ala Glu Asn
60 65

ggc tgt gct gcc gca gcg gga gag ggg ctg gag gat ggt ctg tct tca 351
Gly Cys Ala Ala Ala Ala Gly Glu Gly Leu Glu Asp Gly Leu Ser Ser
70 80 85

tca aat tgt gtt gac gca tct ttg ggt tct gtt tca tca aat gac agt 404
Ser Lys Cys Gly Asp Ala Pro Leu Ala Ser Val Ala Ala Asn Asp Ser
90 95

0010: 42 0011: 2051 0012: DNA 0013: Rattus sp. 0020 0021: CDS 0022: (85)..(1305)

cca ggg cgg aag aag acc aag gta atg act acc aag ggc gcc atc tct 543
 Pro Gly Pro Lys Lys Thr Lys Val Met Thr Thr Lys Gly Ala Ile Ser
 140 145 150

ggc act acc ggc aag gaa gra gaa gca ggg ggc gca atc cag gaa aag 591
 Ala Thr Thr Gly Lys Glu Gly Glu Ala Gly Ala Ala Met Gln Glu Lys
 155 160 165

aag ggg gtg cag aaa gaa aaa aag gca gct gga gga ggg aaa gac gac 639
 Lys Gly Val Gln Lys Glu Lys Lys Ala Ala Gly Gly Gly Lys Asp Glu
 170 175 180 185

act cgt cct aga gcc cct aag atc aat aac tgc atg gac tcc ctg gaa 687
 Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
 190 195 200

gcc atc gat caa gag ctg tca aat gta aat ggc caa gct gac agg gcc 735
 Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
 205 210 215

ttc ctg cag ctg gaa cgc aaa ttt ggg cgg atg aga agg ctg cac atg 783
 Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
 220 225 230

cag cgc cga agt ttc atc atc caa aac atc cca ggt ttc tgg gtc acc 831
 Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
 235 240 245

ggc ttt cgg aac caa cgg caa ctg tca cgg atg atc agt gcc caa gat 879
 Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
 250 255 260 265

gaa gac atg atg agg tac aag atc aat tta gag gtc gag gag ctt aag 927
 Glu Asp Met Met Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
 270 275 280

cac cca aga gca ggg tgc aaa ttt aag ttc atc ttc caa agc aac ccc 975
 His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Ser Asn Pro
 285 290 295

tac ttc cga aat gag ggg ctg gtc aaa gag tac gac cgc aga tcc tca 1023
 Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
 300 305 310

ttt cga gtc ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1071
 Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
 315 320 325

gaa ccc cag gcc cat atc cac agg aat aga gag ggg aac agc att ccc 1119
 Glu Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro
 330 335 340 345

ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 1167
 Ile Ala Glu Ile Ile Lys Gly Val Leu Thr Ser Asn Pro Leu Glu Tyr
 350 355 360 365

tac ctg atg ggc gat ggg cca cgc aga gga gtt cga gtc cca cca agg 1263
 Tyr Leu Met Gly Asp Gly Pro Arg Arg Gly Val Arg Val Pro Pro Arg
 330 385 390

cag cca gtg gag agt ccc agg tcc ttc agg ttc cag tct ggc 1305
 Gln Pro Val Glu Ser Pro Arg Ser Phe Arg Phe Gln Ser Gly
 395 400 405

taagctctgc cctcgtgaga agctcttaca gaagagtcct taccaccttc tcagcttggc 1365

tacgagcatg cagccttctg tatgctttct ctctcttggg ttgtgtcctt tgggtctctt 1425

aagtctcggg tagtttcaag gttgtgggtt ccaagctctt gctctctctt ctcttggcca 1485

tcacgatgta ctgcatagt ttaatgggtg tccaagtga tggcctccaa actgcttcta 1545

tgccaagctc acgtgtgtga gtttgtactg cttctctttg catggcttgg tctctgtctg 1605

tgatcttcta ggttttttgt tttctttttt aaaagtgggt ctctatcaaa agaaagcttg 1665

acatctctt accaagaact agccagattt catactgtgt tccgatata tatgtactgt 1725

gaagaactgt gagtttggcc actgcaagat gggactgtat cccaatccag ccacagccc 1785

aacaggcat tccaagctgt caccaaactga tcttagctgt ctctctgggc ctctgccatt 1845

tacctgctt tttatctata gaatgagcag gtggtctgga ggtgactact aggttaagagt 1905

gaagtattag gtgaggagtg tttctgtgca ccacattgtt ctgttaocaa tgcacatga 1965

tcagcttggg tcagctactg actgtctgat atttctaacc cccaacacaa aaaaaaaaaa 2025

aaaaaaaaa aaaaaaaaaa aaaaaa 2051

<210> 53

<211> 407

<212> FRT

<213> Pattus sp.

<400> 53

Met Asn Gly Val Glu Gly Asn Asn Glu Leu Pro Leu Ala Asn Thr Ser
 1 5 10 15

Thr Ser Ala Leu Val Pro Glu Asp Leu Asp Leu Lys Glu Asp Glu Pro
 20 25 30

Leu Ser Glu Glu Thr Asp Thr Val Arg Glu Met Glu Ala Ala Gly Glu
 35 40 45

Ala Gly Ala Glu Gly Gly Ala Ser Pro Asp Ser Glu His Cys Asp Pro
 50 55 60

Met Asn Gly Val Glu Gly Asn Asn Glu Leu Pro Leu Ala Asn Thr Ser

Ala Gly Pro Leu Ser Pro Ala Lys Pro Lys Thr Leu Glu Ala Ser Gly
115 120 125

Ala Val Gly Leu Gly Ser Gln Met Met Pro Gly Pro Lys Lys Thr Lys
130 135 140

Val Met Thr Thr Lys Gly Ala Ile Ser Ala Thr Thr Gly Lys Glu Gly
145 150 155 160

Glu Ala Gly Ala Ala Met Gln Glu Lys Lys Gly Val Gln Lys Glu Lys
165 170 175

Lys Ala Ala Gly Gly Gly Lys Asp Glu Thr Arg Pro Arg Ala Pro Lys
180 185 190

Ile Asn Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser
195 200 205

Asn Val Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys
210 215 220

Phe Gly Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile
225 230 235 240

Gln Asn Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln
245 250 255

Leu Ser Pro Met Ile Ser Gly Gln Asp Glu Asp Met Met Arg Tyr Met
260 265 270

Ile Asn Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys
275 280 285

Phe Lys Phe Ile Phe Gln Ser Asn Pro Tyr Phe Arg Asn Glu Gly Leu
290 295 300

Val Lys Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser
305 310 315 320

Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala His Ile His
325 330 335

Arg Asn Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser
340 345 350

Asp His Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly
355 360 365

Glu Leu Trp Ser Asn Pro Leu Gln Tyr Tyr Leu Met Gly Asp Gly Pro
370 375 380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (88)..(1329)

<400> 54

gggtgtgtgtg tagacgtttt gggcagagct cggcgctgtc ggaggacaag gaactctccc 60

tcctccacta gtctgaacttc ttccaaa atg agc ggc ctg gat ggg ggc aac aag 114
Met Ser Gly Leu Asp Gly Gly Asn Lys

1 5

ctt cct ctc gcc caa acc ggc ggc ctg gct gct ccc gac cat gcc tca 162
Leu Pro Leu Ala Gln Thr Gly Gly Leu Ala Ala Pro Asp His Ala Ser
10 15 20 25

gga gat ccc gac cta gac cag tgc caa ggg ctg cgt gaa gaa acc gag 210
Gly Asp Pro Asp Leu Asp Gln Cys Gln Gly Leu Arg Glu Glu Thr Glu
30 35 40

gcg aca cag gtg atg ggc aac aca ggt ggg ggc agc ctg gag acc gtt 253
Ala Thr Gln Val Met Ala Asn Thr Gly Gly Gly Ser Leu Glu Thr Val
45 50 55

gca gag ggg ggt gca tcc cag gat cct gtc gac tgt ggc ccc gag ctg 306
Ala Glu Gly Gly Ala Ser Gln Asp Pro Val Asp Cys Gly Pro Ala Leu
60 65 70

ggc gtc cca gtt gcc ggg agt cgc ggc ggt gca gag acc aaa gcc ggg 354
Arg Val Pro Val Ala Gly Ser Arg Gly Gly Ala Ala Thr Lys Ala Gly
75 80 85

cag gag gat gct cca cct tct acg aaa ggt ctg gaa gca gcc tct gcc 402
Gln Glu Asp Ala Pro Pro Ser Thr Lys Gly Leu Glu Ala Ala Ser Ala
90 95 100 105

gcc gag gct gct gac agc agc cag aaa aat ggc tgt cag ctt gga gag 450
Ala Glu Ala Ala Asp Ser Ser Gln Lys Asn Gly Cys Gln Leu Gly Glu
110 115 120

acc agt ggc cct gct ggg cag aag gct cta gaa ggc tgt gga gca ggg 498
Pro Arg Gly Pro Ala Gly Gln Lys Ala Leu Glu Ala Cys Gly Ala Gly
125 130 135

ggc ttg ggg tct cag atg ata ccg ggg aag aag gcc aag gaa gtg acg 546
Gly Leu Gly Ser Gln Met Ile Pro Gly Lys Lys Ala Lys Glu Val Thr
140 145 150

act aaa aaa ctt ctt atc ttg tca gaa ggt taa aat gag gga gaa gaa 594
Thr Lys Lys Arg Ala Ile Ser Ala Ala Val Glu Lys Glu Gly Glu Ala
155 160 165

ttt ttt ttt ttt ttt gag ttt ttt ttg ttt ttt ttt ttt ttt ttt ttt 642
Ala Ala Ala Val Val Gln Gln Thr Arg Pro Arg Ala Pro Arg Ala Arg

aac tgc atg gac tca ctg gag gcc atc gat caa gag ttg tca aac gta	738
Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser Asn Val	
205 210 215	
aat gcc cag gct gac agg gcc ttc ctt cag ctt gag cgc aag ttt ggc	786
Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys Phe Gly	
220 225 230	
cgc atg cga agg ctc cac atg cag cgc aga agt ttc att atc cag aat	834
Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile Gln Asn	
235 240 245	
atc cca ggt ttc tgg gtt act gcc ttt cga aac cac ccc cag ctg tca	882
Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln Leu Ser	
250 255 260 265	
ccg atg atc agt ggc caa gat gaa gac atg ctg agg tac atg atc aat	930
Pro Met Ile Ser Gly Gln Asp Glu Asp Met Leu Arg Tyr Met Ile Asn	
270 275 280	
ttg gag gtg gag gag ctt aaa cac ccc aga gca ggc tgc aaa ttc aag	978
Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys Phe Lys	
285 290 295	
ttc atc ttt cag ggc aac ccc tac ttc cga aat gag ggg ctt gtc aag	1026
Phe Ile Phe Gln Gly Asn Pro Tyr Phe Arg Asn Glu Gly Leu Val Lys	
300 305 310	
gaa tat gaa cgc aga tcc cct ggc cgg gtg gtg cct ctt tcc act cca	1074
Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser Thr Pro	
315 320 325	
atc cgc tgg cac cga ggc caa gac ccc cag gct cat atc cac aga aac	1122
Ile Arg Trp His Arg Gly Gln Asp Pro Gln Ala His Ile His Arg Asn	
330 335 340 345	
cgg gaa ggg aac act atc cct agt ttc ttc aac tgg ttt tca gac cac	1170
Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser Asp His	
350 355 360	
agc ctt cta gaa ttc gac aga att gca gag att atc aaa gga gaa ctg	1218
Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly Glu Leu	
365 370 375	
tgg cct aat cct cta cta caa ttt ttt ttt ttt ttt ttt ttt ttt ttt	1266
Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Met Gly Glu Gly Pro Arg Arg	
380 385 390	
gga att cga ggc cca cca agg cag cca gtg gag aga gcc aga tcc ttc	1314
Gly Ile Arg Gly Pro Pro Arg Gln Pro Val Glu Ser Ala Arg Ser Phe	
395 400 405	

aaaagtcag agcaggaatg agcctgctgt ggctggggt tggaaaggt cacaggaaa 3409
 aacctgcagg atcaggggtg ggaggggagg cccctgaggt gctctccagg gaagagggg 3469
 tggggtttaa atagcatgt tggaggaaga tttctctca atttctcta agtcttgaa 3529
 ttcaccagta gatttttgta aacaaaatgt aagtcgatgt tttctctca ttatcttagg 3589
 agtgacctt atatgtgtg aagattaatg gtatatgctt ctatgtcac tgttttgag 3649
 taaaatccat ttcctttctt tgtttcagcc tatgacaaaa ttgatgttta caggcctgt 3709
 ttttgcttat aattgacaa atgtgacaaa ataccaaatt tgtgtcctgt gcagtatgaa 3769
 gaattcagtg aatattcatt aatgtattag ctgttttgc tctctgttca tatatggctt 3829
 tattcttaga aatataattt gaatgtgac tttcaatagt ctgaatattt tacaaattat 3889
 agctatgtct tgtgaaaaa acctcaaaaa gaaaaaacg acctgttgtt ctacttgat 3949
 atttcttgc ctagtaatgt acttgacatt tatgttcta agcagtgtaa gtaccagtag 4009
 aattctctg tcaaaactaa tgatcattta gtactttgt ctctctccat gtgcttgaag 4069
 gaaaaataaa gtgtcactac cgtatttctt gtttctatca aaaaaataaa ataatttaa 4129
 aaaaaaaaa aaaaaaaaa 4148

<210> 55
 <211> 414
 <212> PRT
 <213> Homo sapiens

<400> 55
 Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly
 1 5 10 15
 Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln
 20 25 30
 Cys Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn
 35 40 45
 Thr Gly Gly Gly Ser Leu Glu Thr Val Ala Glu Gly Gly Ala Ser Gln
 50 55 60
 Asp Pro Val Asp Cys Gly Pro Ala Leu Arg Val Pro Val Ala Gly Ser
 65 70 75 80
 Arg Gly Gly Ala Ala Thr Lys Ala Gly Gln Glu Asp Ala Pro Pro Ser

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

130	135	140
Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser		
145	150	155 160
Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys		
	165	170 175
Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu		
	180	185 190
Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu		
	195	200 205
Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala		
	210	215 220
Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met		
	225	230 235 240
Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr		
	245	250 255
Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp		
	260	265 270
Glu Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys		
	275	280 285
His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Gly Asn Pro		
	290	295 300
Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser		
	305	310 315 320
Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln		
	325	330 335
Asp Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro		
	340	345 350
Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg		
	355	360 365
Ile Ala Gln Ile Ile Lys Gly Glu Leu Trp Ile Asn Ile Leu Gln Tyr		
	370	375 380
Tyr Leu Met Gly Glu Gly Pro Arg Arg Gly Ile Arg Gly Pro Pro Arg		
	385	390 395 400
Gln Pro Val Glu Ser Ala Arg Ser Phe Arg Phe Gln Ser Gly		
	405	410

11/1/77
 11/1/77
 11/1/77

43

345

144

192

243

283

356

384

432

486

576

624

225

230

235

240

caa gtc ctt gtg gca ggc cag aac agg gat tgt gcg ttt cta tgg gaa 764
Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
245 250 255

gac aga ctt tgc tcc agg tta ctg gta tgg cat tgaactggac cagccacagg 801
Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

gcaagcatga cggctctgtg ttgggtgtcc ggtactttac ctgtgccccg aggcacgggg 841

tctttgcacc agcatctagt atccagagga ttgggtggatc cactgatccc cctggagaca 941

gtgttgggagc aaaaaaagtg catcaagtga caatgacaca gcccaaacgc accttcacaa 1001

cagtccggac cccaaaggac attgcacacg agaactctat ctccagggtta ctctctctgt 1061

gtctgtttcc ttggatgtgt agggcgggaga tgcagtctta gagacctgga tacctgacac 1121

agagacagag tccctcttag catctcttga cacaaggaga cccagtcac cctaagatag 1181

agattccacg tgacacctcc agaatagaaa ccccgtttagc cagcctctga ttaactgaggt 1241

cccattatta acagatctcc catgaagcct ccccaaaata cagacctcat gttaccccaa 1301

aagagattcc ctgagtagea ccttcaggtt agtccctgtc cctacccct cagagcagat 1361

ttcccccatt aaacattttc cacatcacc cagggtatgt gacccctccc accacaggac 1421

gtctctgagt taccagtggg tttaggtccc atgaatgaag acccccccac ccccggttct 1481

ccttaagcat aggtccatacc tccagaatag ccagccacat cactatcccc atgtaacatc 1541

agtctctcca aaatggcgtg aggtccatag aaagacctta tactctcttc tcttctctag 1601

agatgccttc catcaactta agtccctgtt ctacccctg aacaagacac ctaattaacc 1661

ggcccaactca cctcaattac aaacaccaaa atcgtcctgg aagcatgaat tacaggacag 1721

caagtcttcc tgcctctctg accttgaga aacccccagt gccttggtatg aagccacccc 1781

caatggccc acagtccctg tctgggccc ggtccaga aaattctcta tcttccaaag 1841

caatctctcc cccctcttg ggggtatct caatttggg gaccccttc tagaacctg 1901

gggagttcaa attccagaga gaatatatat tatatataat ccccaattcc ccatgcttcc 1961

aagccctaca atctctagaa gaccccaaat ttctaattcc caggacttcc cctacccaag 2021

ttatattttt taattctcc cagggtatct caatttggg ataacattcc caaaccttca 2081

caatctctcc cccctcttg ggggtatct caatttggg gaccccttc tagaacctg 2141

caatctctcc cccctcttg ggggtatct caatttggg gaccccttc tagaacctg 2201

caatctctcc cccctcttg ggggtatct caatttggg gaccccttc tagaacctg 2261

caatctctcc cccctcttg ggggtatct caatttggg gaccccttc tagaacctg 2321

attcaattta cattctgggtc acagggtccaa gacactaaat ctgagtcatt ggccccaaag 2441
 gacttcacag caactggggc agactaacag cctgagggag aacctgaggg ccccggtgggt 2501
 ccagagcaga cctggggccc tgaccaccaa ggcagctca cgaactgccc ttcaactgat 2561
 gtccctaacc tcagcatgac tctgtctctc ttcaataaag acgtttctat ggcaaaaaaa 2621
 aaaaaaaaaa aaaaaaaaaa aa 2643

<210> 57
 <211> 267
 <212> PRT
 <213> Rattus sp.

<400> 57

Leu	Lys	Gly	Ala	Arg	Pro	Arg	Val	Val	Asn	Ser	Thr	Cys	Ser	Asp	Phe
1				5					10					15	
Asn	His	Gly	Ser	Ala	Leu	His	Ile	Ala	Ala	Ser	Asn	Leu	Cys	Leu	Gly
		20						25					30		
Ala	Ala	Lys	Cys	Leu	Leu	Glu	His	Gly	Ala	Asn	Pro	Ala	Leu	Arg	Asn
		35					40					45			
Arg	Lys	Gly	Gln	Val	Pro	Ala	Glu	Val	Val	Pro	Asp	Pro	Met	Asp	Met
	50					55					60				
Ser	Leu	Asp	Lys	Ala	Glu	Ala	Ala	Leu	Val	Ala	Lys	Glu	Leu	Arg	Thr
	65				70					75				80	
Leu	Leu	Glu	Glu	Ala	Val	Pro	Leu	Ser	Cys	Thr	Leu	Pro	Lys	Val	Thr
			85						90					95	
Leu	Pro	Asn	Tyr	Asp	Asn	Val	Pro	Gly	Asn	Leu	Met	Leu	Ser	Ala	Leu
		100						105					110		
Gly	Leu	Arg	Leu	Gly	Asp	Arg	Val	Leu	Leu	Asp	Gly	Gln	Lys	Thr	Gly
		115					120					125			
Thr	Leu	Arg	Phe	Cys	Gly	Thr	Thr	Glu	Phe	Ala	Ser	Gly	Gln	Trp	Val
	130					135					140				
Gly	Val	His	Leu	Arg	Glu	Pro	Val	Gly	Lys	Asn	Arg	Gly	Ser	Val	Gly
	145				150					155					160
Gly	Val	Arg	Tyr	Phe	Ile	Cys	Pro	Pro	Lys	Gln	Gly	Leu	Phe	Ala	Ser
			165						170				175		
Val	Ser	Lys	Val	Ser	Lys	Ala	Val	Asp	Ala	Pro	Pro	Ser	Ser	Val	Thr

Gly Arg Arg Val His Lys Gly Lys Lys Lys Ser Thr Ser Ser Thr Thr
 175 180 185 190 195 200 205 210 215 220

Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
245 250 255

Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

```

<210> 58
<211> 2929
<212> DNA
<213> Rattus sp.

```

- (2.20):
- (2.21): CDS
- (2.22): (1) .. (310)

04001-58	ggt gac tct acc tct aga tgg gct gag gcc ctg aga gaa atc tct ggt	48
Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly		
5 10 15		
091 tta gct gaa atg cct gca gat agt gga tac cct gca tac ctt ggt	96	
Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly		
20 25 30		
141 cga cgt gct tct ttc tat gag cga gca ggc aga gtg aaa tgt ctt	144	
Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu		
35 40 45		
191 aac cct gag aga gaa ggg agt gtc agc att gta gga gca gtt tct	192	
Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser		
50 55 60		
241 cct ggt ggt gat ttt tct gat cca gtc aca tct gct act ctg ggt	240	
Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly		
65 70 75 80		
291 att gtt cag gtg ttc tgg ggc ttg gat aag aag cta gct cag cgc aag	283	
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys		
85 90 95		
341 ttc cct tct ctg aac tgg ctg att agc tac ggt aag tac atg ctt	340	
Ile Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Leu Lys Tyr Met Arg		
100 105 110		
391 gcc ctg gac gag tac tat gac aaa cac ttc aca gag ttc gtg cct ctg	384	
Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu		
115 120 125		
441 agg acc aaa gct aag gag att ctg cag gaa gag gag gat ctg gcg gaa	432	
Arg Thr Lys Thr Lys Thr Lys Thr Lys Thr Lys Thr Lys Thr Lys Thr		
130 135 140 145 150 155 160		

165	170	175	
ggg tac aac cct tat gac agg ttr tgt cca ttc tac aag acg gtg ggg			576
Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly			
180	185	190	
atg ctg tcc aac atg att tca ttc tat gat atg gcc cgc cgg gct gtg			624
Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val			
195	200	205	
gag acc acc gcc cag agt gac aat aag atc aca tgg tcc att atc cgt			672
Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg			
210	215	220	
gag cac atg ggg gag att ctc tat aaa ctt tcc tcc atg aaa ttc aag			720
Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys			
225	230	235	240
gat cca gtg aag gat gcc gag gca aag atc aag gcc gac tac gca cag			768
Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln			
245	250	255	
ctt ctt gaa gat atg cag aac gca ttc cgt agc ctg gaa gat			816
Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp			
260	265	270	
tagaactgtg aactctctcc tctctctcgc cagctcatat gtgtatatat tcttgaattt 870			
ctcatctcca accctttgct tccatattgt gcagctttga gactagtgc tctgtcgttc 936			
tcttctatct tctgtttct ttggtaggtc ttataaaaaca cacattcctg tctctcgtg 996			
cttgaaggag ctctgacct ttgtctgaag tgggtgaatgt agtgcatatg atacacagt 1050			
taacatacac attgtaacat atacgtttctg taaacttgta tgtaagggtga ctaccccttc 1110			
cctctctccc agtaaaactgt aaacaggact actgcatgtg ctctattggg gatggaaggc 1170			
cagatctcca taccgtggac aggtacataa ggaaaactaga ccaattgcaa cttagtgttt 1230			
gttgagtaac ctttttgcag gaagtatttc cttttaaaaa acaaaaagatt aatgttccaa 1290			
ctattgtac ctctccagt atcaatcag actgtttgtg ggcacttg gaa tatttt 1350			
gtttctaa cagcgttg caggttga agtaatgat aattcagtt ctttcaaaa 1410			
tgtgaaagta aaaagagagc taggtggtra gaattaaatt gacatcgtct tgtttaagca 1470			
tattttattt cactgagaga tttaatatca aggaatttta tatactcaat tactaggaaa 1530			
tctttctca agtactttt aaactcatt caaatctga tctctatct aacttttc 1590			
cttctctt cctctctctt cctctctctt cctctctctt cctctctctt cctctctctt			
cttctctt cctctctctt cctctctctt cctctctctt cctctctctt cctctctctt			
cttctctt cctctctctt cctctctctt cctctctctt cctctctctt cctctctctt			

aaagaaaaaaa	aagatogatt	tttgtottgc	tgttttggtg	tgtttaaata	ataattccat	1950
atttgcataa	cgaggctcgc	ttctgagagc	ttggagatcg	tgtccctct	tcactctccg	2010
gggtgataat	gctggcgcca	tgtacccct	tcaggagggg	aaggggattg	aacatggcta	2070
acactctcaa	gtacacaagc	gtaacgacaa	agtattttatt	ttaagccttg	gtatgttgtt	2130
taaattatta	ggtaggtgat	ttcttatggc	cttttgggta	gacatagtat	acacttcaga	2190
tgtaatgtgt	aaatccctgc	tagtgcatgt	ctacacgata	gactgctatt	caagaaggat	2250
attcttcac	ataacaattt	aaaaactatt	aaatcagata	tggattatgc	aatgaactgt	2310
tgagaggtgg	attaacgggtg	ctgcttaatc	agtttgcctc	caatatggct	togtatccag	2370
aagccctgac	tagtgagat	gagaaagatt	tcaaaaacctg	ctgcccaca	cttaccagca	2430
acctaggctt	gtgatcagaa	tgaatgatcc	caagaaaacta	cttgcccag	tgtgttttgt	2490
tgtcccggat	ttgagatgtg	cgtttctctc	ccctctgaga	ctgttgatgt	atgagtgtga	2550
agaagttaca	gaaacaacgc	tcagattttc	acggtaactt	tcctctgc	cacactgtag	2610
agttccagat	tgtccactga	tagtgctctc	ttcgtaagga	tgtgttaaaa	tatagcagtc	2670
tttttaaaag	attatgcagt	tcctatttta	ttgtgctgtg	ccgggtcta	agtgcagccg	2730
gttaaaacaag	ttccatatgt	atttttccag	tgttaaactc	catacctatg	cccttggaa	2790
agctccatcc	tgaacaatga	atagaagagg	ctatataaat	tgcctcctta	tccttaagat	2850
ttcactatct	ttatgthaag	agtaatgtat	aattattaaa	atctatgaaa	aataaaaaagt	2910
ggatttaaat	taagagatc					2920

```

<210> 59
<211> 270
<212> PRT
<213> Rattus sp.

```

400 59

Al; As; Ar; Au; Ba; Bi; Br; Ca; Cd; Co; Cr; Cu; Fe; Hg; Hs; In; Ir; K; Kr; La; Li; Lu; Mn; Mo; Na; Nb; Ni; Os; Pb; Pt; Rb; Rh; Ru; S; Se; Si; Sn; Sr; Ta; Te; Ti; Tl; U; V; W; Xe; Zn; Zr

Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
20 25 30

Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
35 40 45

His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg
 100 105 110
 Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
 115 120 125
 Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu
 130 135 140
 Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile
 145 150 155 160
 Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn
 165 170 175
 Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
 180 185 190
 Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
 195 200 205
 Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
 210 215 220
 Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
 225 230 235 240
 Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
 245 250 255
 Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
 260 265 270

<210> 60
 <211> 1489
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1)..(1253)

<400> 1
 gca ctt ctt cgt ggt cgt gag cat gtt gga gag cat ctt ctt ctt 45
 Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser
 1 5 10 15
 ggc cat gag ccc gga tgg tcc gcc cgg att cca gtt ccc cgg att gcc 26
 Gly Pro His Pro His Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
 20 25 30

att ttt att ctt ctt ctt ctt ctt ctt ctt ctt ctt ctt ctt ctt 37
 Glu Arg His Ile His Ile Arg Ile Ile Leu His Ala Arg Gly His Ala

ggg ctc cac cgc cag tct gga agg gtt cca cat aca gga acg gcc tac	240
Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr	
65 70 75 80	
ttc gca gat gag ccc acc gag gct cag gct ccg ggc gga ttc tgc gtg	288
Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val	
85 90 95	
tca ccc tgc ctc ctt ggg gtc cgc tgg ccg gcc tgt gcc acc cgg acg	336
Ser Pro Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr	
100 105 110	
ccc gga tca ctg cct ctg tct ccc cca tca ggc cag ccc cgg acg cta	384
Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu	
115 120 125	
tgg ccc acc cct cca gct ggc ccc tgg agt agg atg gta gca cgt aac	432
Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn	
130 135 140	
cag gtg gca gcc gac aat gag atc tcc ccg gca tca gag ccc cga cgg	480
Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Pro Arg Arg	
145 150 155 160	
cgg cca gag cca tcc tgg tcc tgg tct tgg tcc tgg ccg ggc gcc ccg	528
Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser Pro Ala Ala Pro	
165 170 175	
ggc cgt ccc cgg ccc tgc cca gtg gtc cca gcc ccg gct ccc ggc gac	576
Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp	
180 185 190	
act cac ttc cgc acc ttc cgc tcc cac tct gat tac cgg cgc atc acg	624
Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr	
195 200 205	
cgg acc agc gct ctc ctg gac gcc tgc ggc ttc tac tgg gga ccc ctg	672
Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu	
210 215 220	
agc gtg cat ggg ggc cac gaa cgg ctg cgt gcc gag ccc gtg ggc acc	720
Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr	
225 230 235 240	
ttc ttg tgg cgc gac agt cgt tgg tgg tgg aat ttt ttc ttc tgg ctg agt	768
Phe Leu Val Arg Arg Ser Arg His Arg Asn Cys Ile Ile Ala Leu Ser	
245 250 255	
gtg aag atg gct tgg ggc ccc aag agc att cgt gtg cag ttc cag gcc	816
Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala	
260 265 270	
gac ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc	
His Ile Ile His His Tyr Val Ala Ala His Arg Arg Met Ile Gly Ala	
275 280 285 290	

Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Gln Leu Cys Arg Gln
305 310 315 320

cgc atc gtg gcc gcc gtg ggt cgc gag aac ctg gca cgg atc cct ctt 1008
 Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu
 325 330 335

aac cag gta ctc cgt gac tac ctg agt tcc ttc ccc ttc cag atc 1053
 Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
 340 345 350

tyacgggtg ccgcgtgcc ccagcatta agtgggagc; ccttattatt tcttattatt 1113

attattatt attttttctgg aacccacgtgg gaggcctccc cgcctagggtc ggaggggagtg 1173

jrtg'ggagg gtgagatgcc tcccacttct ggctggagac cttatccgcg ctctcggggg 1233

gattccctc ctggtgctc ctccgggtc ccttggttgt agcagcttgt gtctggggcc 1293

aggactgaa ctccagcgtt acctctccat gtttacaatgt tcccagttatc ttgcacaaaa 1353

ccagcggtgg gggagggtct ctggcttcat tttctgctg tgcagaatat tctattttat 1413

attttacat ccagtttaga taataaaactt tatttatgaaa gttttttttt taaagaaaaa 1473

aaaaaaaaaaaaa 1489

· 410 · 61

511. 351

0212. FRT

0213. *Fattus* sp.

•410• 61

Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser
1 5 10 15

Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
20 25 30

Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu
35 40 45

Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala

(Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr
65 70 75 80

Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val
85 90 95

[illegible]

tag taa tag gag gag gaa gag gag cgt cca cgg cca taa cag gta gta 267
 Ser Ser Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val
 35 40 45
 cag gaa cag ggt cag gga gaa aat caa ttc cga acc ttc cga taa caa 315
 Pro Ala Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His
 50 55 60
 tct gat tac cgg cga atc acg cgg acc agc gct ctc ctg gac gcc tgc 363
 Ser Asp Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys
 65 70 75
 ggc ttc tac tgg gga cca ctg agc gtg cat ggg gag caa gaa cgg ctg 411
 Gly Phe Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu
 80 85 90
 cgt gcc gag cca gtg gga acc ttc ttg gtg cgc gac agt cga cag cgg 459
 Arg Ala Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg
 95 100 105 110
 aac tgc ttc ttc gcg ctg agc gtg aag atg gct tgc ggc cca acg agc 507
 Asn Cys Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser
 115 120 125
 att cgt gtg caa ttc caa gca ggc cgc ttc caa ctg gac ggc agc cgc 555
 Ile Arg Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg
 130 135 140
 gag acc ttc gac tgc ctg ttc gag ctg ctg gag caa tac gtg gcg gcg 603
 Glu Thr Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala
 145 150 155
 cag cgc cgc atg ttg ggg gcc cca ctg cgc cag cgc cgc gtg cgg cgg 651
 Pro Arg Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro
 160 165 170
 ctg cag gag ctg tgt cgc cag cgc atc gtg gcc gcc gtg ggt cgc gag 699
 Leu Gln Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu
 175 180 185 190
 aac ctg gca cgc atc cct ctt aac cag gta ctc cgt gac tac ctg agt 747
 Asn Leu Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser
 195 200 205
 tcc tta ccc ttc caa atc taaggtta cccctttta cccctttta 795
 Ser Phe Pro Phe Gln Ile
 210
 agtggggagcg ccttattatt ccttattatt aattattatt attttttcgg aaaaagtg 855
 gacccctttt cccctttttt agggggagta gttgagggg gtagatgca taaacttt 915

tatttatgaaa gttttttttt taaaaaadaaa aaaaaaaa

1194

<210> 63
<211> 212
<212> FRT
<213> Rattus sp.

<400> 63
Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
1 5 10 15
Ser Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser
20 25 30
Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala
35 40 45
Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
50 55 60
Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe
65 70 75 80
Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
85 90 95
Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys
100 105 110
Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
115 120 125
Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
130 135 140
Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
145 150 155 160
Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
165 170 175
Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
180 185 190
Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
195 200 205
Pro Phe Gln Ile
210

<210> 63

1194
1195
1196

400 64

tttccaaaga	ctgcagcgcc	ttagggccca	ggtttcaaca	gattcctcaa	aatg cca	57
					Met Pro	
					1	
tcg caa atg gag cat gcc atg gaa acc atg atg ctt aca ttt cac agg	105					
Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe His Arg						
5 10 15						
ttt gca ggg gaa aaa aac tac ttg acg aag gag gac ctg aga gtg ctc	153					
Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu						
20 25 30						
atg gaa agg gag ttc cct ggg ttt ttg gaa aat caa aag gac cct ctg	201					
Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp Pro Leu						
35 40 45 50						
gct gtg gac aaa ata atg asa gac ctg gac bag tgc cga gat gga aaa	249					
Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp Gly Lys						
55 60 65						
gtg ggc ttc bag agc ttt cta tca cta gtg ggg ggg ctg atc att gca	297					
Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile Ile Ala						
70 75 80						
tgc aat gac tat ttt gta gta cac atg aag cag aag aag taggccaaact	346					
Cys Asn Asp Tyr Phe Val Val His Met Lys Gln Lys Lys						
85 90 95						
ggagaccttg taaccacacc ttgatggctc ctctcccattg gggccaactg aggaatctgc	406					
ccccctgctt cctgtgagca gacaggacc cttaggaaaat gtgcataataa catccaactc	466					
caattcgaca agcagagaaa gaaaagttaa tccaatgaca gaggagcttt cgagtttttat	526					
attgittgca tcgggttgcc ctcaataaag aaagtctttt tttttaagtt ccgaaaaaaaa	586					
aaaaaiaaaa aaaa	600					

210> 65

22 95

2125 INT

(213) $\text{Ra}^{+} + \text{us} \rightarrow \text{sr}$.

• **•**

Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe
1 5 10 15

His Arg Phe Ala Gly Gln Lys Asn Tyr Leu Thr Lys Gln Arg Leu Arg
20 35 50

90

```

(210)> 66
(211)> 639
(212)> DNA
(213)> Rattus sp.

```

```

(220>
(221> CDS
(222> 1)..(636)

```

```

0400> 66
atg gcg tac gcc tat ctc ttc aag tac atc atc atc ggc gac aca ggt    48
Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
      1           5           10           15

```

gtt ggt aaa tcy tcy tta ttg cta cag ttt aca gac aag agg ttt cag 96
Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Cln
20 25 30

ccc gtc cat gag ctg aca att ggt gta gag ttt ggt gct cga atg ata 144
 Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
 35 40 45

acc att gat ggg aaa cag ata aaa ctc cag atc tgg gat aca gca ggg 192
Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
50 55 60

gag gag tcc ttt cgt tct atc aca agg tca tat tac aga ggt gca gag 240
 Gln Gln Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75 80

ggg ggt tta cta gtg tat gat att aca agg aga gac acg ttc aac cac 288
Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
85 90 95

ttg aca acc tgg tta gaa gac gcc cgt cag cat tcc aat tcc aac atg 336
Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
100 105 110

Arg Arg Arg Cys Arg Gln Asn Asn Arg Gln Thr Gln Trp Arg Gln Gln 384
 Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Gln Ser Arg Arg Gln
 116 120

dtg aaa aag gaa gaa ggt gaa gct ttt gca cga gag cat gga ctt atc 432
 Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
 130 135 140

The Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe

gac acc aat gca tct cac gga ggc aac caa gga ggg gag gag gca ggg 624
 Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly
 195 200 205

gga ggc tgc tgc tga 639
 Gly Gly Cys Cys
 210

<210> 67
 <211> 212
 <212> PRT
 <213> Rattus sp.

<400> 67
 Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
 1 5 10 15

Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
 20 25 30

Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
 35 40 45

Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
 50 55 60

Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75 80

Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
 85 90 95

Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
 100 105 110

Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu
 115 120 125

Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
 130 135 140

Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe
 145 150 155 160

Ile Asn Thr Ala Lys Glu Ile Tyr Glu Lys Ile Gln Glu Gly Val Phe
 165 170 175

Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala
 180 185 190

195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300

195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)...(613)

<400> 68

atg gtg ctg ctc aag gaa tat cgg gtc atc ctg cct gtg tct gta gat	48
Met Val Leu Leu Lys Glu Tyr Arg Val Ile Leu Pro Val Ser Val Asp	
1 5 10 15	
gag tat caa gtg ggg cag ctg tac tct gtg gct gaa gcc agt aaa aat	96
Glu Tyr Gln Val Gly Gln Leu Tyr Ser Val Ala Glu Ala Ser Lys Asn	
20 25 30	
gaa act ggt ggt ggg gaa ggt gtg gag gtc ctg gtg aac gag ccc tac	144
Glu Thr Gly Gly Gly Gln Gly Val Glu Val Leu Val Asn Glu Pro Tyr	
35 40 45	
gag aag gat gat ggc gag aaa ggc cag tac aca cac aag atc tac cac	192
Glu Lys Asp Asp Gly Gln Lys Gly Gln Tyr Thr His Lys Ile Tyr His	
50 55 60	
tta cag agc aaa gtt ccc aag ttt gtt cga atg ctg gcc cca gaa ggc	240
Leu Gln Ser Lys Val Pro Thr Phe Val Arg Met Leu Ala Pro Glu Gly	
65 70 75 80	
gcc ctg aat ata cat gag aaa gcc tgg aat gcc tac cct tac tgc aga	288
Ala Leu Asn Ile His Glu Lys Ala Trp Asn Ala Tyr Pro Tyr Cys Arg	
85 90 95	
acc gtt att aca aat gag tac atg aag gaa gac ttt ctc att aaa att	336
Thr Val Ile Thr Asn Glu Tyr Met Lys Glu Asp Phe Leu Ile Lys Ile	
100 105 110	
gaa acc tgg cac aag cca gac ctt ggc acc cag gag aat gtg cat aaa	384
Glu Thr Trp His Lys Pro Asp Leu Gly Thr Gln Glu Asn Val His Lys	
115 120 125	
ctg gag cct gag gca tgg aaa cat gtg gaa gct ata tat ata gac atc	432
Leu Glu Pro Glu Ala Trp Lys His Val Glu Ala Ile Tyr Ile Asp Ile	
130 135 140	
ggt gtt cca at cca cca ttt att aag tat tat aag gta tgg aca gac	480
Ala Asp Arg Ser Gln Val Leu Ser Lys Asp Tyr Lys Ala Glu Glu Asp	
145 150 155 160	
cca gca aaa ttt aaa tct atc aaa aca gga cga gga cca ttg ggc cgg	528
Pro Ala Lys Phe Lys Ser Ile Lys Thr Gly Arg Gly Pro Leu Gly Pro	
165 170 175	
ggt ttt att cca ttt cca ttt cca ttt cca ttt cca ttt cca ttt cca	576
Gly Phe Asn Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
180 185 190 195 200 205 210 215 220 225 230 235 240	
Ala Lys Lys Leu Val Val Val Lys Thr Lys Thr Thr Lys Thr Thr Asn	584
245 250 255 260 265 270 275 280 285 290 295 300	

Lys Val Glu Asn Phe Ile His Lys Gln Glu Lys Arg Leu Phe Thr Asn
 210 215 220

tat cac agg cag ctg ttc tgt tgg ctt gat aaa tgg gtt gat ctg act 720
 Phe His Arg Gln Leu Phe Cys Trp Leu Asp Lys Trp Val Asp Leu Thr
 225 230 235 240

atg gat gac att cgg agg atg gaa gaa gag acg aag aga cag ctg gat 768
 Met Asp Asp Ile Arg Arg Met Glu Glu Glu Thr Lys Arg Gln Leu Asp
 245 250 255

gag atg aga caa aag gac ccc gtg aaa gga atg aca gca gat gac tag 816
 Glu Met Arg Gln Lys Asp Pro Val Lys Gly Met Thr Ala Asp Asp
 260 265 270

(210): 69

(211): 2263

(212): DNA

(213): Simian sp.

(400): 69

cgtctctctc ctccccttctc tctagcagta gcctctcttaa tctagctttaa tggctttaca 60

aagaaagcca ggcagaggag caattctcag tggctgtggt cggaccatga cctagctgac 120

catgaacttg gaagggcttg aaatgatagc agttctgacg gtcattgtgc tttttgttaa 180

atatttgga cagtttgggc tgattgaagc aggtttagaa gacagcgttg aagatgaact 240

ggagatggcc atgtctagggc atgggcctga ggccttgag cttctgggaag cccagagcaa 300

attaccaag aaagagcttc agatccttta cagaggattt aagaacgaat gcccagtggt 360

tgttgtaaat gaagaaacct tcaaagagat ttactcagag ttctttccac agggagactc 420

tacaacatat gcacatttctc tgttcaatgc gtttgatacg gaccacaatg gagctgtgag 480

tttcgaggat ttcacaaag gtctttccat ttctctcagg gggacagtac aagaaaaact 540

caattgggca tttaatctgt atgatataaa taaagatggc tacatcaact aagaggaaat 600

gttgatata atgaaagcaa tctcagat gatgggtaaa tgtaaatat ctgtctcaca 660

agaagatga atagagaa atctgaaac atttttctc aaattgggtc aaatataaga 720

tgggtttgtt accatagatg agttcattga aagctgccc aaagatgaaa acataatggg 780

ctccatgcag ctctttgaaa atgtgattta acttgctaac tagatcctga atcccaacaga 840

aaatgtgaa ctattttaa acatttaag tggatgat caattttaa atagattgtt 900

ttttttaa atagattgtt atctttaa atctttaa atctttaa atctttaa atctttaa

atctttaa atctttaa atctttaa atctttaa atctttaa atctttaa atctttaa

atctttaa atctttaa atctttaa atctttaa atctttaa atctttaa atctttaa 114

taatataactg acatctgcac ttaatttcaa gaaattaaat taattctcat gcttgaatga 1260
 tgaatttcaa tttatatact ttaagtaaac aaataagatt actacaatta aacacatagt 1320
 tcaagtttct atggccttca ctcccaact totattagaa attaatctta totgggtatt 1380
 ttaaacattt aaaaatttat catcagatat cagcatatgc ctaattatgc ctaatgaaac 1440
 ttaataagca ttttaatttc catcatabat tatagtcaag gcttatatac tatatataat 1500
 ttgggatttg ttttaatttc caggtctgtt tccattgtat catcaagtgg aagttcaaga 1560
 cggcatcaaa caaaacaagg atgtttacag acatatgcaa aggttcagga tatctatcct 1620
 ccagtatatg ttaatgotta ataacaagta atctaacag cattaaaggc caaatctgtc 1680
 ctcttctccc tgacttctt acagcatgtt tatattacaa gccattcagg gacaaagaaa 1740
 ccttgaactac ccactgtct actaggaaca aacaaacagc aagcaaat cactttgaac 1800
 gcaccagtggt ttccattaca ttgacaaact ctaccaagat tcagttagaa ataagtgtct 1860
 aacaaactaat ccagattaca atatgattta gtgcacata aaattccaac aattcagatt 1920
 atttttaact aactcagcaa caactgtaaa gttgcacat tactaaagac acacacatcg 1980
 tccctgtttt gttagaaatat caaaaagacc aagaggtcac agaaggagga aatttgcaac 2040
 tgtctttgca acaataaact aggtatctat totggtgtag agataggatg ttgaaagctg 2100
 cctgtctatc accagtgtag aaattaagag tagtacaata catgtacact gaaatttgcc 2160
 atcgctgttt tgtgtaaaat caatgtgcac attttgtatt tcaaaaaagaa aaaataaaaag 2220
 aaaaataaaa tgtttataac tctaaaaaaa aaaaaaaaaa aaa 2283

<210> 79

<211> 229

<212> PRT

<213> Simian sp.

<400> 70

Met Asn Leu His Gly Leu Glu Met Ile Ala Val Leu Ile Val Ile Val
 1 5 10

Leu Phe Val Lys Leu Leu Glu Gln Phe Gly Leu Ile Glu Ala Gly Leu
 20 25 30

Glu Asp Ser Val Glu Asp Glu Leu Ala Met Ala Thr Val Arg His Arg
 35 40

Val Leu Val Leu Leu Tyr Arg Tyr Leu Tyr Asp Glu Tyr Ile Val Gly
 45 50

85

90

95

Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp
100 105 110

Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu
115 120 125

Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe
130 135 140

Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met
145 150 155 160

Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr
165 170 175

Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe
180 185 190

Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr Ile Asp Glu Phe
195 200 205

Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu
210 215 220

Phe Glu Asn Val Ile
225

(210): 71
(211): 2259
(212): DNA
(213): Simian sp.

(400): 71
gtcgacagac gccctggccc ggtggactcc tgagtcttac tcttgcaacc tgggtcccca 60
gaca'gaatg tgaggagagt ggaaagcatt tgggtccagc tggaggaggc cagctccaca 120
ggcgutttcc tgtatgctca gaacagcacc aagcgcagca ttaaagagcg gctcatgaag 180
ctcttgccct gctcagctgc caaaacatcg tctctctta ttcaaaacag cgtggaaat 240
gaatgaga tctctctgt tctctctgt tctctctgt tctctctgt tctctctgt 300
agcaaatcta caaagaaaga gcttcagatc cttacagag gatttaagaa cgaatgccc 360
agtgggtgtg ttaatgaaga aaccttcaaa gagatttact cgcagttctt tccacaggga 420
gactctacaa catatgcaca tttctctct tctctctct tctctctct tctctctct 480
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 540

gctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 600
tctctctct tctctctct tctctctct tctctctct tctctctct tctctctct 660

atgagctcca tgcagctctt tgaaaatgtg atttaacttg tcaactagat cctgaatcca 840
acagacaaat gtgaactatt ctaccacct taaagtccga gctaccactt ttagcataga 900
ttgctcagct tgacaatgaa goaatattatg caaacaagct ttgttttaat ataaagcaat 960
ccccaaaaga ttgagtttct tcagttataa atttgcacct ttccataat gccactgagt 1020
tcatgggatg ttctgaacta ttccatactc tgtgaatatt caaaagtaat agaattctggc 1080
atatagrrtt attgattcct tagccatggg attattgagg ctttcacata tcagtcatct 1140
taaaatacca gtgttttttg ctactcattt gctatgtatc agtcttagga ttttgaatgg 1200
ttttcctaata tactgacatc tgcatttaat ttccagaaat taaattaatt ttcatgtctg 1260
aatgtctgaa ttccatttat atactttaag taaacaaata agattactac aattaaacac 1320
atagttccag ttcttatggc cttcacttcc cactttctat tagaaattaa ttttatctgg 1380
tatttttaaa catttaaaaa ttctacatca gatatcagca tatgcctaatt tatgcctaatt 1440
gaaacttaat aagcatttaa ttctacatca tacattatag tcaaggcata tatactatat 1500
ataattttgg atttgtttta tcttacaggc tgttttccat tgtatcaca agtggaagtt 1560
caagaaggca tcaaacaaaa caaggatggt tacagacata tgcaaaaggt caggatatct 1620
atctccagct atatgttaat gcttaataac aagtaactct aacagcatta aaggccaaat 1680
ctgtctctct tcccttgact tcttacagc atgttttatat tacaagccat tcagggacaa 1740
agaaacottg actaccccac tgtctactag gaacaaacaa acagcaagca aaattcactt 1800
tgaaagcacc agtgggttcc ttacattgac aactactacc aagattccagt agaaaataag 1860
tgctcaacaa ctaatccaga ttacaatatg atttagtgcg tcataaaaatt ccaacaatto 1920
agattatttt taatcacctc agccacaaat gtaaagttgc cacattacta aagacacaca 1980
catcgtccct gttttgtaga aatatcacia agaccaagag gctacagaag gagaaaaatt 2040
gcaactgtct ttgaacaaat aaatcaggtc tctattcttg tttgacata gttttttaa 2100
agctgctctc tctacaaat tttacaaat tttacaaat tttacaaat tttacaaat 2160
ttgccatcgc gtgtttgtgt aaactcaatg tgcacatttt gtatttcaaa aagaaaaaat 2220
aaaagcaaaa taaaatgtta aaaaaaaaaa aaaaaaaaaa 2280

2280

10/1/00
Mr. Andrew Rhodes, Esq. 1000 10th Ave. S.W. 5th Fl. Apt. 501
Seattle, WA 98101

Ser Ser Thr Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser
20 25 30

Ile Lys Glu Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr
35 40 45

Ser Ser Pro Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala
50 55 60

Thr Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser
65 70 75 80

Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn
85 90 95

Glu Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr
100 105 110

Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu
115 120 125

Phe Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp
130 135 140

Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys
145 150 155 160

Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile
165 170 175

Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met
180 185 190

Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His
195 200 205

Val Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val
210 215 220

Thr Ile Asp Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met
225 230 235 240

Arg Ser Met Gln Leu Phe Glu Asn Val Ile
245 250

<210> 73

<211> 11

<212> FRT

<213> Simian sp.

<400> 73

Ser Asn Ala Lys Ala Val Glu Thr Asp Val
1 4 10